

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 20:50:35 ; Search time 128 Seconds
(without alignments)
869.717 Million cell updates/sec

Title: US-09-989-728-422
Perfect score: 2067
Sequence: 1 MFCPLKLLLPVLLDYSGL.....RNNSLKSGGMPKTTQAP 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2067	100.0	394	3	AAY66764 Membrane-
2	2067	100.0	394	3	AAB33454 Human PRO
3	2067	100.0	394	3	AAY94452 Human inf
4	2067	100.0	394	3	AAB24433 Human PRO
5	2067	100.0	394	4	AAL12431 Human PRO
6	2067	100.0	394	4	AAM38860 Human pol
7	2067	100.0	394	4	AAB65287 Human PRO
8	2067	100.0	394	5	AAB84933 Human PRO
9	2067	100.0	394	5	ABB95539 Human ang
10	2067	100.0	394	5	ABU58102 Human PRO
11	2067	100.0	394	6	ABU59180 Novel hum
12	2067	100.0	394	6	ABU2692 Human sec
13	2067	100.0	394	6	ABU17875 Novel hum
14	2067	100.0	394	6	ABU60611 Human sec
15	2067	100.0	394	6	ABU80836 Human PRO
16	2067	100.0	394	6	ABU33802 Novel hum
17	2067	100.0	394	6	ABU13993 Human PRO
18	2067	100.0	394	6	ABU81129 Human PRO
19	2067	100.0	394	6	ABU72578 Novel hum
20	2067	100.0	394	6	ABU66829 Human PRO
21	2067	100.0	394	6	ABU59910 Novel sec
22	2067	100.0	394	6	ABU59327 Human sec
23	2067	100.0	394	6	ABO26024 Human PRO
24	2067	100.0	394	6	ABO25100 Human sec
25	2067	100.0	394	6	ABO25100 Human sec

26	2067	100.0	394	6	ABU82145 Novel hum
27	2067	100.0	394	6	ABU59033 Human sec
28	2067	100.0	394	6	ABU92411 Novel hum
29	2067	100.0	394	6	ABU59476 Novel hum
30	2067	100.0	394	6	ABU67105 Human sec
31	2067	100.0	394	6	ABU92242 Novel hum
32	2067	100.0	394	6	ABU10948 Human PRO
33	2067	100.0	394	6	ABU81700 Novel hum
34	2067	100.0	394	6	ABU88639 Human sec
35	2067	100.0	394	6	ABO34153 Human PRO
36	2067	100.0	394	6	ADA46039 Novel hum
37	2067	100.0	394	6	ADA76470 Human PRO
38	2067	100.0	394	6	ABJ72325 Human PRO
39	2067	100.0	394	6	ADA19120 Human PRO
40	2067	100.0	394	6	ADA61743 Homo sapi
41	2067	100.0	394	6	ADB19528 Novel hum
42	2067	100.0	394	6	ADB28069 Human PRO
43	2067	100.0	394	6	ADA86548 Novel hum
44	2067	100.0	394	6	ADB16112 Human PRO
45	2067	100.0	394	6	ADA37933 Human sec

ALIGNMENTS

RESULT 1
AAY66764
ID AAY66764 standard; protein; 394 AA.
XX
AC AAY66764;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1387.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.

PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-009057P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 98US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR N-PSDB; AA265110.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 12; Fig 304; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWILS 60
|||
Db 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWILS 60

Db 61 PGEHAKDEYVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQEQADQGTVICEIRL 120
Qy 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
Db 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
Qy 181 IVFRIYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRIYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
Qy 241 LVFKKTIIVLHVSPEEPRTLVTTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKTCTC 300
Db 241 LVFKKTIIVLHVSPEEPRTLVTTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKTCTC 300
Qy 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIIVREVIEEEEPSEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIIVREVIEEEEPSEKSEAT 360
Qy 361 YMTMHPVWPVPSLRDRNNSLEKSGGMPKTOQAF 394
Db 361 YMTMHPVWPVPSLRDRNNSLEKSGGMPKTOQAF 394

RESULT 3

AAAY94452
ID AAAY94452 standard; protein; 394 AA.
XX
AC AAAY94452;
DT 11-SEP-2000 (first entry)
XX
DE Human inflammation associated protein #11.
XX
KW Inflammation; rheumatoid arthritis; Crohn's disease; asthma;
KW multiple sclerosis; allergy; AIDS; diabetes mellitus antiinflammatory;
KW gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO200029574-A2.
XX
PD 25-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026234.
XX
PR 18-NOV-1998; 98US-00195292.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Walker MG, Volkmut W, Klingler TM;
XX
DR WPI; 2000-387787/33.
DR N-PSDB; AAA27133.
XX
PT New human inflammation-associated polypeptide useful for diagnosis,
PT prevention and treatment of inflammatory diseases comprises product of
PT gene coexpressed with e.g. CD16, L-selectin and IP-30.
XX
PS Claim 4; Page 42-43; 43pp; English.

CC Eleven novel inflammation-associated genes have been identified in cDNA
CC libraries from various tissues. The genes were selected according to
CC their coexpression with the known inflammation genes, CD16, L-selectin,
CC Src-like adapter protein, IP-30, superoxide dismutase subunits, alpha-
CC 1-antitrypsin, C1q-A, 5-lipoxygenase activating protein and SRC family
CC tyrosine kinase. The novel polynucleotides may be used in hybridization
CC assays to diagnose a disease or condition associated with altered
CC expression of the inflammation genes. Antibodies against the genes may be
CC useful in compositions for the diagnosis and treatment of such diseases
CC associated with inflammation including rheumatoid arthritis, Crohn's
CC disease, multiple sclerosis, AIDS, diabetes mellitus, asthma and allergy.
CC Additionally the polynucleotides of the invention may be used for gene
CC therapy. The present sequence is human inflammation associated protein

CC #11, derived from Incyte Clone 3507924
XX
SQ Sequence 394 AA;
Query Match 100.0%; Score 2067; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFCEPLKLIILLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIPIKIDWTLS 60
Db 1 MFCEPLKLIILLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIPIKIDWTLS 60
Qy 61 PGEHAKDEYVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQEQADQGTVICEIRL 120
Db 61 PGEHAKDEYVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQEQADQGTVICEIRL 120
Qy 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
Db 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
Qy 181 IVFRIYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRIYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
Qy 241 LVFKKTIIVLHVSPEEPRTLVTTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKTCTC 300
Db 241 LVFKKTIIVLHVSPEEPRTLVTTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKTCTC 300
Qy 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIIVREVIEEEEPSEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPPIIVREVIEEEEPSEKSEAT 360
Qy 361 YMTMHPVWPVPSLRDRNNSLEKSGGMPKTOQAF 394
Db 361 YMTMHPVWPVPSLRDRNNSLEKSGGMPKTOQAF 394

RESULT 4

AAAB24433
ID AAAB24433 standard; protein; 394 AA.
XX
AC AAAB24433;
DT 07-NOV-2000 (first entry)
XX
DE Human PRO1387 protein sequence SEQ ID NO:220.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.

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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77683.
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX Claim 72; Fig 92; 315pp; English.
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX Sequence 394 AA;
SQ

Query Match 100.0%; Score 2067; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLLPVLLDYSGLNDLNSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLLLPVLLDYSGLNDLNSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILNDGSLLLQDVQADQGTIYCEIRL 120
Db 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILNDGSLLLQDVQADQGTIYCEIRL 120
QY 121 KGESQVFKKAVVHLVLPPEPKELMVHVGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
Db 121 KGESQVFKKAVVHLVLPPEPKELMVHVGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIIVLHVSPEEPTLTVPALRPLVLGGNQLVIVGIVCATILLPVLIVKKTTC 300
Db 241 LVFKKTIIVLHVSPEEPTLTVPALRPLVLGGNQLVIVGIVCATILLPVLIVKKTTC 300
QY 301 GNKSSVNSTLVKNTKTNPEIKKPCFCHFERCEGKHIIYPIIVREVEIEEPEPSEKSEAT 360
Db 301 GNKSSVNSTLVKNTKTNPEIKKPCFCHFERCEGKHIIYPIIVREVEIEEPEPSEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNSLEKSGGMPKTOQAF 394
Db 361 YMTMHPVWPSLRSDRNSLEKSGGMPKTOQAF 394

RESULT 5
AAU12431

ID AAU12431 standard; protein; 394 AA.
XX AC AAU12431;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO1387 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US032678.
XX PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US015264.
PR 02-JUN-2000; 2000US-0209832P.
PR 05-JUN-2000; 2000WO-US020710.
PR 28-JUL-2000; 2000WO-US022031.
PR 11-AUG-2000; 2000WO-US023522.
PR 23-AUG-2000; 2000WO-US023328.
PR 24-AUG-2000; 2000WO-US030952.
PR 08-NOV-2000; 2000WO-US030873.
PR 10-NOV-2000; 2000WO-US030873.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21503.
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,

PT breast, prostate, cervical.
XX Claim 12; Fig 520; 813pp; English.
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQVQADQGTTCIRL 120
Db 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQVQADQGTTCIRL 120
QY 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVEWIFSGRAKEE 180
Db 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVEWIFSGRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIIVHVSPEEPTLTPAALRPLVLGGNQLVIVGIVCATILLPLVLIVKKT 300
Db 241 LVFKKTIIVHVSPEEPTLTPAALRPLVLGGNQLVIVGIVCATILLPLVLIVKKT 300
QY 301 GNKSSVNSTVLVKNKTNPKEIKPCHFERCEGEKHIYSPPIVREVIEEPEPSEKSEAT 360
Db 301 GNKSSVNSTVLVKNKTNPKEIKPCHFERCEGEKHIYSPPIVREVIEEPEPSEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTTQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTTQAF 394

RESULT 6
ID AAM38860 standard; protein; 394 AA.
XX AAM38860;
AC AAM38860;
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 2005.
DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX Homo sapiens.
OS WO200153312-A1.
XX 26-JUL-2001.
PD 26-DEC-2000; 2000WO-US034263.
XX 23-DEC-1999; 99US-00471275.
PF 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR N-PSDB; AAI58016.
DR Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
PS Example 3; SEQ ID NO 2005; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQVQADQGTTCIRL 120
Db 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQVQADQGTTCIRL 120
QY 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVEWIFSGRAKEE 180
Db 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVEWIFSGRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240

PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX Claim 12; Fig 304; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytotstatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGNDLVNPPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLLPVLDDYSLGNDLVNPPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEYLVYYNSLNSVPPIGFQNRVHLMGDIICNDGSLLDQVQEQADQGTICEIRL 120
Db 61 PGEHAKDEYLVYYNSLNSVPPIGFQNRVHLMGDIICNDGSLLDQVQEQADQGTICEIRL 120
QY 121 KGESQVFKKAVLHVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
Db 121 KGESQVFKKAVLHVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
QY 181 IVFRIYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIH LGN 240
Db 181 IVFRIYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIH LGN 240
QY 241 LVFKKTIIVLHVSPEEPTLVTAPALRPLVLGGNQLVILVIVGIVCATILLPVLILIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPTLVTAPALRPLVLGGNQLVILVIVGIVCATILLPVLILIVKKT 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPERCEGEKHIYSPPIIVREVIEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPERCEGEKHIYSPPIIVREVIEEPESEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTTQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTTQAF 394

RESULT 8
AAU83689
ID AAU83689 standard; protein; 394 AA.
XX
AC AAU83689;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 196.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.

QY 241 LVFKKTIIVLHVSPEEPTLVTAPALRPLVLGGNQLVILVIVGIVCATILLPVLILIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPTLVTAPALRPLVLGGNQLVILVIVGIVCATILLPVLILIVKKT 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPERCEGEKHIYSPPIIVREVIEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPERCEGEKHIYSPPIIVREVIEEPESEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTTQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTTQAF 394

RESULT 7
AAB65287
ID AAB65287 standard; protein; 394 AA.
XX
AC AAB65287;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1387 (UNQ722) protein sequence SEQ ID NO:422.
XX
KW Human; secreted and transmembrane protein; PRO; cytotstatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.

(GETH) GENENTECH INC.
XX
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44256.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive

XX PD 31-JAN-2002.
XX PF 29-JUN-2001; 2001WO-US021066.
XX PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX (GETH) GENENTECH INC.
XX PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX DR WPI; 2002-172001/22.
XX N-PSDB; ABK33633.
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX Claim 11; Fig 196; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60

QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEIRL 120
Db 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEIRL 120
QY 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
Db 121 KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRAKEE 180
QY 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIIVLHVSPEEPRTLVTPLALRPLVLGGNQLVIVGIVCATILLPLVILIVKKTCTC 300
Db 241 LVFKKTIIVLHVSPEEPRTLVTPLALRPLVLGGNQLVIVGIVCATILLPLVILIVKKTCTC 300
QY 301 GNKSSVNSTVLVKNTKKTNPKEIKPKCHFERCEGEKHIYSPILIVREVIEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKKTNPKEIKPKCHFERCEGEKHIYSPILIVREVIEEPESEKSEAT 360
QY 361 YMTMHPVWPSLRSRDNNSLEKSGGMPKTOQAF 394
Db 361 YMTMHPVWPSLRSRDNNSLEKSGGMPKTOQAF 394
RESULT 9
ID ABB84933
XX ABB84933 standard; protein; 394 AA.
AC ABB84933;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1387 protein sequence SEQ ID NO:234.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.

XX (GETH) GENENTECH INC.

PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.
DR N-PSDB; ABL88188.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 234; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention

XX Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKILLLPVLLDYSGLNDLNVSPPELTTHVHVSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKILLLPVLLDYSGLNDLNVSPPELTTHVHVSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQEAQGTYYICEIRL 120
Db 61 PGEHAKDEVLYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQEAQGTYYICEIRL 120
QY 121 KGESQVFKKAVVHLVPEEPKELMHVGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
Db 121 KGESQVFKKAVVHLVPEEPKELMHVGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
QY 181 IVFRYYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIH LGN 240
Db 181 IVFRYYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIH LGN 240
QY 241 LVFKKTIIVLHVSPEEPTLTVPALRPLVLGGNQLVIIIGIVCATILLPLVILIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPTLTVPALRPLVLGGNQLVIIIGIVCATILLPLVILIVKKT 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPILIVREVIEEERPESEKSEAT 360

Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPILIVREVIEEERPESEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSKGGMPKTKQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSKGGMPKTKQAF 394

RESULT 10

ABB95539

ID ABB95539 standard; protein; 394 AA.

XX ABB95539;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO1387 SEQ ID NO: 234.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 30-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 30-MAY-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017800.

XX 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95677.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 234; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db |||||
Qy 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db |||||
Qy 61 PGEHAKDEYVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQVQADQGTTCIRL 120
Db |||||
Qy 61 PGEHAKDEYVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQVQADQGTTCIRL 120
Db |||||
Qy 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRABE 180
Db |||||
Qy 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWIFSGRRABE 180
Db |||||
Qy 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHGN 240
Db |||||
Qy 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHGN 240
Db |||||
Qy 241 LVFKKTIHLVSPPEPRTLVTPAALRPLVLGNLQVIVGIVCATILLPVLILIVKKTTC 300
Db |||||
Qy 241 LVFKKTIHLVSPPEPRTLVTPAALRPLVLGNLQVIVGIVCATILLPVLILIVKKTTC 300
Db |||||
Qy 301 GNKSSVNSTVLVKNTKTNPEIKEKPFCEGEKHIYSPPIVREVEIEEPEEPESEAT 360
Db |||||
Qy 301 GNKSSVNSTVLVKNTKTNPEIKEKPFCEGEKHIYSPPIVREVEIEEPEEPESEAT 360
Db |||||
Qy 361 YMTMHPVWPSLRSDRNNSLEKKS GGMPKTOQAF 394
Db |||||
Qy 361 YMTMHPVWPSLRSDRNNSLEKKS GGMPKTOQAF 394
Db |||||

RESULT 11
ABU58102
ID ABU58102 standard; protein; 394 AA.
XX
AC ABU58102;
XX

DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #134.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.

PR	23-JUN-1998;	98US-0090355P.	PR	26-AUG-1998;	98US-0098014P.
PR	24-JUN-1998;	98US-0090429P.	PR	31-AUG-1998;	98US-0098525P.
PR	24-JUN-1998;	98US-0090431P.	PR	16-SEP-1998;	98US-0100634P.
PR	24-JUN-1998;	98US-0090435P.	PR	16-SEP-1998;	98WO-US019330.
PR	24-JUN-1998;	98US-0090444P.	PR	17-SEP-1998;	98US-0100858P.
PR	24-JUN-1998;	98US-0090445P.	PR	17-SEP-1998;	98WO-US019437.
PR	24-JUN-1998;	98US-0090472P.	PR	07-OCT-1998;	98WO-US021141.
PR	24-JUN-1998;	98US-0090535P.	PR	01-DEC-1998;	98WO-US025108.
PR	24-JUN-1998;	98US-0090540P.	PR	22-DEC-1998;	98US-0113296P.
PR	24-JUN-1998;	98US-0090542P.	PR	05-JAN-1999;	99WO-US000106.
PR	24-JUN-1998;	98US-0090557P.	PR	08-MAR-1999;	99WO-US005028.
PR	25-JUN-1998;	98US-0090676P.	PR	12-MAR-1999;	99US-0123957P.
PR	25-JUN-1998;	98US-0090678P.	PR	02-JUN-1999;	99WO-US012252.
PR	25-JUN-1998;	98US-0090690P.	PR	23-JUN-1999;	99US-0141037P.
PR	25-JUN-1998;	98US-0090694P.	PR	07-JUL-1999;	99US-0143048P.
PR	25-JUN-1998;	98US-0090695P.	PR	20-JUL-1999;	99US-0144758P.
PR	25-JUN-1998;	98US-0090696P.	PR	26-JUL-1999;	99US-0145698P.
PR	26-JUN-1998;	98US-0090862P.	PR	28-JUL-1999;	99US-0146222P.
PR	26-JUN-1998;	98US-0090863P.	PR	17-AUG-1999;	99US-0149396P.
PR	01-JUL-1998;	98US-0091360P.	PR	15-SEP-1999;	99WO-US021090.
PR	01-JUL-1998;	98US-0091544P.	PR	15-SEP-1999;	99WO-US021547.
PR	02-JUL-1998;	98US-0091478P.	PR	08-OCT-1999;	99US-0158663P.
PR	02-JUL-1998;	98US-0091519P.	PR	30-NOV-1999;	99WO-US028313.
PR	02-JUL-1998;	98US-0091628P.	PR	01-DEC-1999;	99WO-US028301.
PR	02-JUL-1998;	98US-0091628P.	PR	01-DEC-1999;	99WO-US028634.
PR	02-JUL-1998;	98US-0091646P.	PR	16-DEC-1999;	99WO-US030095.
PR	02-JUL-1998;	98US-0091673P.	PR	20-DEC-1999;	99WO-US030911.
PR	07-JUL-1998;	98US-0091978P.	PR	05-JAN-2000;	2000WO-US000219.
PR	07-JUL-1998;	98US-0091982P.	PR	06-JAN-2000;	2000WO-US000376.
PR	09-JUL-1998;	98US-0092182P.	PR	11-FEB-2000;	2000WO-US003565.
PR	10-JUL-1998;	98US-0092472P.	PR	18-FEB-2000;	2000WO-US004341.
PR	20-JUL-1998;	98US-0093333P.	PR	22-FEB-2000;	2000WO-US004414.
PR	30-JUL-1998;	98US-0094651P.	PR	24-FEB-2000;	2000WO-US004914.
PR	04-AUG-1998;	98US-0095282P.	PR	24-FEB-2000;	2000WO-US005004.
PR	04-AUG-1998;	98US-0095285P.	PR	02-MAR-2000;	2000WO-US005841.
PR	04-AUG-1998;	98US-0095301P.	PR	10-MAR-2000;	2000WO-US006319.
PR	04-AUG-1998;	98US-0095302P.	PR	15-MAR-2000;	2000WO-US006884.
PR	04-AUG-1998;	98US-0095318P.	PR	20-MAR-2000;	2000WO-US007377.
PR	04-AUG-1998;	98US-0095321P.	PR	30-MAR-2000;	2000WO-US008439.
PR	04-AUG-1998;	98US-0095325P.	PR	15-MAY-2000;	2000WO-US013358.
PR	10-AUG-1998;	98US-0095929P.	PR	17-MAY-2000;	2000WO-US013705.
PR	10-AUG-1998;	98US-0096012P.	PR	22-MAY-2000;	2000WO-US014042.
PR	11-AUG-1998;	98US-0096143P.	PR	30-MAY-2000;	2000WO-US014941.
PR	11-AUG-1998;	98US-0096146P.	PR	02-JUN-2000;	2000WO-US015264.
PR	12-AUG-1998;	98US-0096329P.	PR	23-JUN-2000;	2000US-0213637P.
PR	17-AUG-1998;	98US-0096757P.	PR	28-JUL-2000;	2000WO-US020710.
PR	17-AUG-1998;	98US-0096766P.	PR	11-AUG-2000;	2000WO-US022031.
PR	17-AUG-1998;	98US-0096768P.	PR	23-AUG-2000;	2000WO-US023522.
PR	17-AUG-1998;	98US-0096773P.	PR	24-AUG-2000;	2000WO-US023328.
PR	17-AUG-1998;	98US-0096791P.	PR	07-SEP-2000;	2000US-0230978P.
PR	17-AUG-1998;	98US-0096867P.	Query Match 100.0%; Score 2067; DB 6; Length 394;		
PR	17-AUG-1998;	98US-0096891P.	Best Local Similarity 100.0%; Pred. No. 5.le-188;		
PR	17-AUG-1998;	98US-0096894P.	Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
PR	17-AUG-1998;	98US-0096895P.	Qy	1	MFCPLKLLLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDWTLS 60
PR	17-AUG-1998;	98US-0096897P.	Db	1	MFCPLKLLLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDWTLS 60
PR	18-AUG-1998;	98US-0096949P.	Qy	61	PGEHAKDEYVLYYSNLSPVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTICEIRL 120
PR	18-AUG-1998;	98US-0096950P.	Db	61	PGEHAKDEYVLYYSNLSPVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTICEIRL 120
PR	18-AUG-1998;	98US-0096959P.	Qy	121	KGESQVFKKAVLVHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWFIFSRRAKEE 180
PR	18-AUG-1998;	98US-0096960P.	Db	121	KGESQVFKKAVLVHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWFIFSRRAKEE 180
PR	18-AUG-1998;	98US-0097022P.	Qy	181	IVFRYHKLKRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRESDDGNYTCSIHLGN 240
PR	20-AUG-1998;	98US-0097218P.	Db	181	IVFRYHKLKRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMQLGVRESDDGNYTCSIHLGN 240
PR	26-AUG-1998;	98US-0097952P.	Qy	241	LVFKKTTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIIGVICATILLPLVILIVKKT 300
PR	26-AUG-1998;	98US-0097954P.			
PR	26-AUG-1998;	98US-0097955P.			
PR	26-AUG-1998;	98US-0097971P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0097978P.			
PR	26-AUG-1998;	98US-0097979P.			
PR	26-AUG-1998;	98US-0097986P.			

Db 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNGQLVIIVGIVCATILLPLVLILIVKKTG 300

QY 301 GKKSSVNSTVLVKNTKKTNPEIKKPKCHFERCEGKHYSPIIIVREVIEEEEPSEKSEAT 360

Db 301 GKKSSVNSTVLVKNTKKTNPEIKKPKCHFERCEGKHYSPIIIVREVIEEEEPSEKSEAT 360

QY 361 YMTMHPVWPVPSLSDRNNSLEKSGGMPKTKQAF 394

Db 361 YMTMHPVWPVPSLSDRNNSLEKSGGMPKTKQAF 394

RESULT 12

ABU59180

ID ABU59180 standard; protein; 394 AA.

XX

AC ABU59180;

XX

DT 28-APR-2003 (first entry)

XX

DE Novel human secreted or transmembrane protein PRO1387.

XX

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;

KW vascular endothelial growth factor inhibition; VEGF inhibition;

KW endothelial cell growth inhibitor; T-lymphocyte stimulation;

KW retinal neurons cell survival; rod photoreceptor cell survival;

KW retinal disorder; retinitis pigmentosa; kidney disorder;

KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;

KW chondrocyte redifferentiation; sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2002132252-A1.

XX

PD 19-SEP-2002.

XX

PF 14-NOV-2001; 2001US-00990442.

XX

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088036P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 97US-0049787P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088036P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

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PR 10-JUN-1998; 97US-0049787P.

PR 11-JUN-1998; 98US-0088858P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089440P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089532P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089599P.

PR 17-JUN-1998; 98US-0089600P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 06-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006319.

PR 20-MAR-2000; 2000WO-US006884.

PR 30-MAR-2000; 2000WO-US007377.

PR 15-MAY-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013358.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 28-AUG-2001; 2001US-00941992.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX

DR WPI; 2003-247083/24.

DR N-PSDB; ABX80392.

XX

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346

PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 12; Fig 304; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCFKIDWTLS 60
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Qy 61 PGEHAKDEVLYYYSNLSVPGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGYICEIRL 120
Db 61 PGEHAKDEVLYYYSNLSVPGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGYICEIRL 120
Qy 121 KGESQVFKKAVLVHLVPEEPKELMHVVGGLIQMGCVFQSTEVKHVTKVWFISGRRAKEE 180
Db 121 KGESQVFKKAVLVHLVPEEPKELMHVVGGLIQMGCVFQSTEVKHVTKVWFISGRRAKEE 180
Qy 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIHLGN 240
Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIHLGN 240
Qy 241 LVFKKTIIVLHVSPEEPRTLVTAAALRPLVLGGNQLVIIIVGIVCATILLPLVILLIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPRTLVTAAALRPLVLGGNQLVIIIVGIVCATILLPLVILLIVKKT 300
Qy 301 GNKSSVNSTVLVNTKTKTNPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEKSEAT 360
Db 301 GNKSSVNSTVLVNTKTKTNPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEKSEAT 360
Qy 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394

ID ABU82692 standard; protein; 394 AA.
XX AC ABU82692;
XX DT 26-JUN-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO1387.
XX KW Human; PRO; secreted protein; transmembrane protein; wound healing;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US2003032023-A1.
XX PD 13-FEB-2003.
XX PF 14-NOV-2001; 2001US-00990711.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088028P.
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PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 16-JUN-1998; 98US-0089514P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.

PR	19-JUN-1998;	96US-0089947P;
PR	19-JUN-1998;	98US-0089948P;
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PR	24-JUN-1998;	98US-0090557P;
PR	25-JUN-1998;	98US-0090676P;
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PR	25-JUN-1998;	98US-0090690P;
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PR	07-JUL-1998;	98US-0091982P;
PR	09-JUL-1998;	98US-0092182P;
PR	10-JUL-1998;	98US-0092437P;
PR	20-JUL-1998;	98US-0093339P;
PR	30-JUL-1998;	98US-0094651P;
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PR	04-AUG-1998;	98US-0095301P;
PR	04-AUG-1998;	98US-0095302P;
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PR	10-AUG-1998;	98US-0095916P;
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PR	10-AUG-1998;	98US-0096012P;
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PR	17-SEP-1998;	98WO-US019437;
PR	07-OCT-1998;	98WO-US021141;
PR	01-DEC-1998;	98WO-US025108;
PR	22-DEC-1998;	98US-0113296P;
PR	05-JAN-1999;	99WO-US000106;
PR	08-MAR-1999;	99WO-US005028;
PR	12-MAR-1999;	99US-0123957P;
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PR	15-SEP-1999;	99WO-US021547;
PR	08-OCT-1999;	99US-0158663P;
PR	30-NOV-1999;	99WO-US028313;
PR	01-DEC-1999;	99WO-US028301;
PR	16-DEC-1999;	99WO-US028634;
PR	20-DEC-1999;	99WO-US030095;
PR	05-JAN-2000;	99WO-US030911;
PR	06-JAN-2000;	2000WO-US000219;
PR	11-FEB-2000;	2000WO-US000376;
PR	18-FEB-2000;	2000WO-US003565;
PR	22-FEB-2000;	2000WO-US004341;
PR	24-FEB-2000;	2000WO-US004414;
PR	24-FEB-2000;	2000WO-US004914;
PR	02-MAR-2000;	2000WO-US005004;
PR	10-MAR-2000;	2000WO-US005841;
PR	15-MAR-2000;	2000WO-US006319;
PR	20-MAR-2000;	2000WO-US006884;
PR	30-MAR-2000;	2000WO-US007377;
PR	15-MAY-2000;	2000WO-US008439;
PR	17-MAY-2000;	2000WO-US013358;
PR	22-MAY-2000;	2000WO-US013705;
PR	30-MAY-2000;	2000WO-US014941;
PR	02-JUN-2000;	2000WO-US015264;
PR	23-JUN-2000;	2000US-0213637P;
PR	28-JUL-2000;	2000WO-US020710;
PR	11-AUG-2000;	2000WO-US022031;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0

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Db	1	MFCPLKLI	LLPVL	LDYSL	GLNDL	NVSPPE	LTVH	VGDSAL	MGCVFQ	STEDK	CIFKID	WTLS	60
QY	61	PGEHAKDE	YVLYXY	SNLSV	PIGRFQ	NRVH	LMGDI	LCDGSL	LLQDVQ	EADQ	GTIY	CEIRL	120
Db	61	PGEHAKDE	YVLYXY	SNLSV	PIGRFQ	NRVH	LMGDI	LCDGSL	LLQDVQ	EADQ	GTIY	CEIRL	120
QY	121	KGESQVFK	AAVVLH	VLPPEE	PKELMV	HVGG	LIQM	GCVFQ	STEVKH	VTKEW	IFSG	RRAKEE	180
Db	121	KGESQVFK	AAVVLH	VLPPEE	PKELMV	HVGG	LIQM	GCVFQ	STEVKH	VTKEW	IFSG	RRAKEE	180
QY	181	IVFRYTH	KLRMS	VEYSQ	SWGHFQ	NRVNL	VGDI	IFRNDG	SIMLQ	GVRES	DGGNYT	CSIH	240
Db	181	IVFRYTH	KLRMS	VEYSQ	SWGHFQ	NRVNL	VGDI	IFRNDG	SIMLQ	GVRES	DGGNYT	CSIH	240

Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRES DGNVTC SIHLGN 240

QY 241 LVFKKTIVLHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVL IIVKKT C 300

Db 241 LVFKKTIVLHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVL IIVKKT C 300

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Db 301 GNKSSVNSTVLVKNTKTNPEIKPKPCHFERCEGEKHIYSP IIVREVIEEEEPSEKSEAT 360

QY 361 YMTMHPVWPVPSLRSDRNNLSLEKSGGMPKTQQAF 394

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RESULT 14

ABO17875

ID ABO17875 standard; protein; 394 AA.

XX AC ABO17875;

XX 26-AUG-2003 (first entry)

DT Novel human secreted and transmembrane protein PRO1387.

XX Human; secreted and transmembrane protein; PRO; antiinflammatory;

KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;

KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;

KW TNF-alpha release; cell proliferation; cell differentiation;

KW gene expression modulator; proteoglycan release; cytokine release;

KW tumour; inflammatory disease; organ failure; atherosclerosis;

KW cardiac injury; infertility; birth defect; premature aging; AIDS;

KW acquired immunodeficiency syndrome; cancer; diabetic complication;

KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;

KW bioreactor; tissue typing.

XX Homo sapiens.

OS US2003032156-A1.

PN 13-FEB-2003.

XX 06-MAY-2002; 2002US-00140474.

XX 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

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PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 22-DEC-1999; 99WO-US030720.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

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PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

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PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 18-MAY-2001; 2001US-00860216.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001US-00872035.

PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.

PR 14-JUN-2001; 2001US-00882636.

PR 19-JUN-2001; 2001US-00886342.

PR 20-JUN-2001; 2001WO-US019692.

PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.

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PR 09-JUL-2001; 2001WO-US021735.

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PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.

PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

XX PA XX

PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

DR WPI; 2003-288106/28.
DR N-PSDB; ABX90370.

XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.

PS Claim 12; Fig 304; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent

CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. NO. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLIILPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MFCPLKLIILPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGEHAKDEYVLYYNSLSPICRQNRVHLMGDLICNDGSLLLQDVQEAQGTYICEIRL 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 PGEHAKDEYVLYYNSLSPICRQNRVHLMGDLICNDGSLLLQDVQEAQGTYICEIRL 120
QY 121 KGESQVFKKAVVHLVPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVWEVIFSGRRAKEE 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 KGESQVFKKAVVHLVPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVWEVIFSGRRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRESGGNYTCSIH LGN 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRESGGNYTCSIH LGN 240
QY 241 LVFKKTIIVLHVSPEEPRTLVTPALRLPLVLGNGNLVIVGIVCATILLPLVLIIVKKTTC 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 LVFKKTIIVLHVSPEEPRTLVTPALRLPLVLGNGNLVIVGIVCATILLPLVLIIVKKTTC 300
QY 301 GNKSSVNSTVLVKNTKKTNPKEKPCFCHFERCEGEKHIYSP IIVREVIEEPEPSEKSEAT 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 GNKSSVNSTVLVKNTKKTNPKEKPCFCHFERCEGEKHIYSP IIVREVIEEPEPSEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKKS GGGMPKTTQAF 394
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 YMTMHPVWPSLRSDRNNLSLEKKS GGGMPKTTQAF 394

Search completed: October 1, 2004, 21:04:10
Job time : 135 secs

25/01/2025

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 19:36:10 ; Search time 943 Seconds
(without alignments)
7343.121 Million cell updates/sec

Title: US-09-989-728-421
Perfect score: 1630
Sequence: 1 cggctcgagtcagctgtgg.....taaaaacccaacccaatacaa 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1630	100.0	1630	3	Aaz65110 Membrane-
2	1630	100.0	1630	3	Aaa77683 Human PRO
3	1630	100.0	1630	4	Aas21503 Human CDN
4	1630	100.0	1630	5	Aaf44256 Human PRO
5	1630	100.0	1630	6	Abk33633 cDNA enco
6	1630	100.0	1630	6	AbL88188 Human PRO
7	1630	100.0	1630	6	AbL95677 Human ang
8	1630	100.0	1630	7	Abx77981 Human PRO
9	1630	100.0	1630	7	Abx80393 Novel hum
10	1630	100.0	1630	7	ACA69299 Human cDN
11	1630	100.0	1630	7	ACD24112 Novel hum
12	1630	100.0	1630	7	Abx90370 Human sec
13	1630	100.0	1630	7	ACA66938 cDNA enco
14	1630	100.0	1630	7	ACD68690 Novel hum
15	1630	100.0	1630	7	ABX64216 cDNA enco
16	1630	100.0	1630	7	ACA67253 cDNA enco
17	1630	100.0	1630	7	ACA64438 Novel hum
18	1630	100.0	1630	7	ACA03862 cDNA enco
19	1630	100.0	1630	7	ABX89400 DNA enco
20	1630	100.0	1630	7	ABX80897 Human sec
21	1630	100.0	1630	7	ACD44406 cDNA enco
22	1630	100.0	1630	7	ACD42054 Human sec
23	1630	100.0	1630	7	ACA68594 Novel hum

24	1630	100.0	1630	7	ABX79577	Abx79577 Human sec
25	1630	100.0	1630	7	ACA93598	Aca93598 Novel hum
26	1630	100.0	1630	7	ABX81280	Abx81280 Novel hum
27	1630	100.0	1630	7	ACA04283	Aca04283 Human CDN
28	1630	100.0	1630	7	ACA93096	Aca93096 Novel hum
29	1630	100.0	1630	7	ABX17180	Abx17180 Human PRO
30	1630	100.0	1630	8	ACA68035	Aca68035 Novel hum
31	1630	100.0	1630	8	ACA88484	Aca88484 Human sec
32	1630	100.0	1630	8	ACD81991	AcD81991 cDNA enco
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34	1630	100.0	1630	8	ADA76469	Ada76469 Human PRO
35	1630	100.0	1630	8	ABT44323	Abt44323 Human PRO
36	1630	100.0	1630	8	ADA19119	Ada19119 Human PRO
37	1630	100.0	1630	8	ADA61742	Ada61742 Homo sapi
38	1630	100.0	1630	8	ADB19527	Adb19527 Novel hum
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42	1630	100.0	1630	8	ADA37932	Ada37932 Human CDN
43	1630	100.0	1630	8	ADA47897	Ada47897 Human PRO
44	1630	100.0	1630	8	ADA21618	Ada21618 Human cDN
45	1630	100.0	1630	8	ADA10405	Ada10405 Human CDN

ALIGNMENTS

RESULT 1
AAZ65110
ID AAZ65110 standard; cDNA; 1630 BP.
XX
AC AAZ65110;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1387 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 05-JUN-1998; 98US-0088655P.
PR 09-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
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PR 10-JUN-1998; 98US-0088824P.
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PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
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PR 19-JUN-1998; 98US-0089952P.
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PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
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PR 24-JUN-1998; 98US-0090445P.
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PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
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PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
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PR 02-JUL-1998; 98US-0091478P.
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PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.

PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
DR P-PSDB; AAY66764.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
XX
PS Claim 2; Fig 303; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCTCGAGTCAGCTGTGGGAGATTTCAGTCAGTCCTCCCTGGGTGCTCTTCATC 60

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1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCCTCCCTGGTGCTCTTCATC 60
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61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCCTGCTGCCAGTG 120
121 TTA CTGGATTA TTTCC TTGGGCTGAATGACTTGAATGTTTCCAGACGACAGAAATGTATA 180
121 TTA CTGGATTA TTTCC TTGGGCTGAATGACTTGAATGTTTCCAGACGACAGAAATGTATA 180
181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAATGTATA 240
181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAATGTATA 240
241 TTCAAGATPAGACTGGACTCTGTCAACAGGAGACGCGCAAGGACGAATATGTCTATAC 300
241 TTCAAGATPAGACTGGACTCTGTCAACAGGAGACGCGCAAGGACGAATATGTCTATAC 300
301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGTATGGG 360
301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGTATGGG 360
361 GACATCTTATGCAATCGCCCTCTCTCCTGCTCCAAAGATGTGCAAGAGGCTGACCAAGGA 420
361 GACATCTTATGCAATCGCCCTCTCTCCTGCTCCAAAGATGTGCAAGAGGCTGACCAAGGA 420
421 ACCTATATCTGTGAAATCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAGCGGTGTTA 480
421 ACCTATATCTGTGAAATCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAGCGGTGTTA 480
481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTTCCATGTGGTGGATGATTTCAG 540
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601 TCAGGACGGCGCGCAAGGAGGAGATTGTTTTCGTTACTACCACAACTCAGGATGTCT 660
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QY 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCCTTCTCTGAGG 1200
QY 1201 TCAGATCGGAACAACTCACTTGAAAAAAGTCAAGTGGGGAATGCCAAAAACACAGCAA 1260
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QY 1261 GCCTTTTGAGAAGAAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
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Db 1321 TGTGTCTCTGGGCCACTCTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
QY 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGACTGGAC 1440
Db 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGGAACAGGCTGTGAGGGAGGGAGGAGCATGGACTTGGCCTCTGGAGTGG 1500
Db 1441 AGCTCTGGAGGAACAGGCTGTGAGGGAGGGAGGAGCATGGACTTGGCCTCTGGAGTGG 1500
QY 1501 ACACCTGGCCCTGGGAACAGGCTGAGCTGAGTGGCTCAAAACCCCTGGATCAGACC 1560
Db 1501 ACACCTGGCCCTGGGAACAGGCTGAGCTGAGTGGCTCAAAACCCCTGGATCAGACC 1560
QY 1561 CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA 1620
Db 1561 CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 2

AAA77683

ID AAA77683 standard; cDNA; 1630 BP.

XX AAA77683;

AC AAA77683;
XX 07-NOV-2000 (first entry)

DT Human PRO1387 cDNA sequence SEQ ID NO:219.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytosolic; gene therapy; vaccine; ss.

OS Homo sapiens.

XX WO200032221-A2.

PN 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1998; 98WO-US025108.

PR 16-DEC-1998; 98US-0112850P.

PR 12-JAN-1999; 99US-0115554P.

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR P-PSDB; AAB24433.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
PS Claim 61; Fig 91; 315pp; English.
XX
CC The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA7721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATGCTCCCTCGGTGCTCTTCATC 60
DB 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATGCTCCCTCGGTGCTCTTCATC 60
QY 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGTCGCAGTG 120
DB 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGTCGCAGTG 120
QY 121 TTACTGGATTATTCCTTGGCCCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
DB 121 TTACTGGATTATTCCTTGGCCCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
QY 181 CATGTGGGTGATTTCAGCTCTGATGGGATGTTTTCAGAGCAGCAGCAAGCAATATGATA 240
DB 181 CATGTGGGTGATTTCAGCTCTGATGGGATGTTTTCAGAGCAGCAGCAAGCAATATGATA 240
QY 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGACGAATATGCTATAC 300
DB 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGACGAATATGCTATAC 300
QY 301 TATTACTCCAATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTTGTGGGG 360
DB 301 TATTACTCCAATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTTGTGGGG 360
QY 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA 420
DB 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA 420
QY 421 ACCTATATCTGTGAATCCGCCCTCAAAGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTTA 480

Db 421 ACCTATATCTGTGAATCCGCCCTCAAAGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTTA 480
QY 481 CTGCATGTGCTTCCAGAGAGCCCAAAGAGCTCATGGTCCATGTGGGTGATTTGATTCAG 540
Db 481 CTGCATGTGCTTCCAGAGAGCCCAAAGAGCTCATGGTCCATGTGGGTGATTTGATTCAG 540
QY 541 ATGGGATGTGTTTCCAGAGCAGAGAAAGTGAACACACGTGACCAAGGTAGATATTT 600
Db 541 ATGGGATGTGTTTCCAGAGCAGAGAAAGTGAACACACGTGACCAAGGTAGATATTT 600
QY 601 TCAGGACGGCGCGCAAAGAGGAGATTTGATTTTCGTTACTACCAAACTCAGGATGTCT 660
Db 601 TCAGGACGGCGCGCAAAGAGGAGATTTGATTTTCGTTACTACCAAACTCAGGATGTCT 660
QY 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
Db 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
QY 721 TTCCGCAATGACGGTTCATCATGCTTCAAGAGTGGGGAGTCAGATGGAGAAACTAC 780
Db 721 TTCCGCAATGACGGTTCATCATGCTTCAAGAGTGGGGAGTCAGATGGAGAAACTAC 780
QY 781 ACCTGCAGTATCCACCTAGGAAACCTGGTGTCAAGAAACCAATGTGCTGCATGTGAGC 840
Db 781 ACCTGCAGTATCCACCTAGGAAACCTGGTGTCAAGAAACCAATGTGCTGCATGTGAGC 840
QY 841 CCGGAAGAGCTCGAACACTGCTGACCCCGGAGCCCTGAGGCTCTGGTCTGGGTGGT 900
Db 841 CCGGAAGAGCTCGAACACTGCTGACCCCGGAGCCCTGAGGCTCTGGTCTGGGTGGT 900
QY 901 AATCAGTTGGTGCATCATTTGTTGGGAATTTCTGTGCCACAATCTGCTGCTCCCTGTTCTG 960
Db 901 AATCAGTTGGTGCATCATTTGTTGGGAATTTCTGTGCCACAATCTGCTGCTCCCTGTTCTG 960
QY 961 ATATTGATCGTGAAGAAGACCTGTGGAAATAGAGTTCAGTGAATTTACAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAAGACCTGTGGAAATAGAGTTCAGTGAATTTACAGTCTTGGTG 1020
QY 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT 1080
Db 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT 1080
QY 1081 GAAGGGGAGAAACACATTTACTCCCAATAATTTGTACGGGAGGTGATCGAGGAAGAAGAA 1140
Db 1081 GAAGGGGAGAAACACATTTACTCCCAATAATTTGTACGGGAGGTGATCGAGGAAGAAGAA 1140
QY 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGG 1200
QY 1201 TCAGATCGGAACAACTCACTTGAAGAAAAAGTCAAGTGGGGAAATGCAAAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACAACTCACTTGAAGAAAAAGTCAAGTGGGGAAATGCAAAAAACACAGCAA 1260
QY 1261 GCCTTTTGAAGAAGATGGAGATCCCTTCACTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
Db 1261 GCCTTTTGAAGAAGATGGAGATCCCTTCACTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
QY 1321 TGTGTCCTGGGCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT 1380
Db 1321 TGTGTCCTGGGCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT 1380
QY 1381 CTCATTGTTTGTGTCATACACTGAAGATGGAGAAATTTGGAGCCCTGGCAGAGAGACTGGAC 1440
Db 1381 CTCATTGTTTGTGTCATACACTGAAGATGGAGAAATTTGGAGCCCTGGCAGAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGGCTCTGGAGTGGG 1500
Db 1441 AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGGCTCTGGAGTGGG 1500
QY 1501 ACACCTGGCCCTGGGAACAGGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACC 1560

Db 1501 AACTGGCCCTGGGAACACAGGCTGAGCTGAGTGGCTCAAAACCCCGTTGGATCAGACC 1560
QY 1561 CTCCTGTGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
Db 1561 CTCCTGTGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 3
AAS21503
ID AAS21503 standard; cDNA; 1630 BP.
XX
AC AAS21503;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO1387 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR P-PSDB; AAU12431.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 3; Fig 519; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 4; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCAATTGCTCCCTCCCTGGTGCTTTCATC 60
Db 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCAATTGCTCCCTCCCTGGTGCTTTCATC 60
QY 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG 120
Db 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG 120
QY 121 TTACTGGATTATTCCTTGGGCTGATGAGTGAATGTTTCCCGCTGAGCTAACAGTC 180
Db 121 TTACTGGATTATTCCTTGGGCTGATGAGTGAATGTTTCCCGCTGAGCTAACAGTC 180
QY 181 CATGTGGTGATTTCAGTCTGTATGGGATGTGTTTCCAGAGCACAGAACAAATGTATA 240
Db 181 CATGTGGTGATTTCAGTCTGTATGGGATGTGTTTCCAGAGCACAGAACAAATGTATA 240
QY 241 TTCAGATAGACTGACTCTGTCCAGGAGAGCAGCCCAAGGACCAATATGTGCTATAC 300
Db 241 TTCAGATAGACTGACTCTGTCCAGGAGAGCAGCCCAAGGACCAATATGTGCTATAC 300
QY 301 TATTACTCCAAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCGCTACACTTGTATGGG 360
Db 301 TATTACTCCAAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCGCTACACTTGTATGGG 360
QY 361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA 420
Db 361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA 420
QY 421 ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTTCAAGAGCGGTGGTA 480

Db 421 ACCTATATCTGTGAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTA 480
QY 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGCTCCATGCTGGGTGGATTGATTCAG 540
Db 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGCTCCATGCTGGGTGGATTGATTCAG 540
QY 541 ATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACAGTGAACCAAGTAGAATGGATATT 600
Db 541 ATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACAGTGAACCAAGTAGAATGGATATT 600
QY 601 TCAGGACGGCGCGCAAGAGGAGATGTTATTTTCGTTACTACCAAACTCAGGATGTCT 660
Db 601 TCAGGACGGCGCGCAAGAGGAGATGTTATTTTCGTTACTACCAAACTCAGGATGTCT 660
QY 661 GTGAGTACTCCAGAGCTGGGGCCACTTCCAGAACTGTGTGAACCTGGTGGGGACATT 720
Db 661 GTGAGTACTCCAGAGCTGGGGCCACTTCCAGAACTGTGTGAACCTGGTGGGGACATT 720
QY 721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC 780
Db 721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC 780
QY 781 ACCTGCAGTATCCACCTAGGGAACCTGTGTTCAAGAAACCAATTGTGCTGCATGTGAGC 840
Db 781 ACCTGCAGTATCCACCTAGGGAACCTGTGTTCAAGAAACCAATTGTGCTGCATGTGAGC 840
QY 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCCTCTGGTCTTGGGTGGT 900
Db 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCCTCTGGTCTTGGGTGGT 900
QY 901 AATCAGTTGGTGATCATTTGTGGGAATTTGTGTGCCACAATCTGCTGCTCCCTGTTCTG 960
Db 901 AATCAGTTGGTGATCATTTGTGGGAATTTGTGTGCCACAATCTGCTGCTCCCTGTTCTG 960
QY 961 ATATTGATCGTGAAGAACCTGTGGAATAAGAGTTCAAGTGAATTTACAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAACCTGTGGAATAAGAGTTCAAGTGAATTTACAGTCTTGGTG 1020
QY 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
Db 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
QY 1081 GAAGGGAGAAACACATTTACTCCCAATAATTGTACGGAGGTGATCGAGGAAGAAGAA 1140
Db 1081 GAAGGGAGAAACACATTTACTCCCAATAATTGTACGGAGGTGATCGAGGAAGAAGAA 1140
QY 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200
QY 1201 TCAGATCGAAACAACTCACTTGAATAAAGTCAGGTGGGGGAATGCCAAAACACAGCAA 1260
Db 1201 TCAGATCGAAACAACTCACTTGAATAAAGTCAGGTGGGGGAATGCCAAAACACAGCAA 1260
QY 1261 GCCTTTTGAAGAAGATGGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
Db 1261 GCCTTTTGAAGAAGATGGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
QY 1321 TGTGTCTGGGCCACTCTACAGTGAATTTTCAAGTCTCCGCTCTCCAGTGTCTCTCTGT 1380
Db 1321 TGTGTCTGGGCCACTCTACAGTGAATTTTCAAGTCTCCGCTCTCCAGTGTCTCTCTGT 1380
QY 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
Db 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGAACAGGCCCTGTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
Db 1441 AGCTCTGGAGAACAGGCCCTGTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
QY 1501 AACTGGCCCTGGGAACAGGCTGAGTGGCCTCAAACCCCGTGGATCAGACC 1560

Db 1501 AACTGGCCCTGGGAACCAAGGCTGAGCTGAGTGGCTCAAAACCCCGTGGATCAGACC 1560
QY 1561 CTCCTGTGGCAGGGTTCCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA 1620
Db 1561 CTCCTGTGGCAGGGTTCCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 4
AAF44256

ID AAF44256 standard; cDNA; 1630 BP.

XX AAF44256;

XX 02-APR-2001 (first entry)

XX Human PRO1387 (UNQ722) nucleotide sequence SEQ ID NO:421.

XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US008439.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 07-JUL-1999; 99US-0143048P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 17-AUG-1999; 99US-0149396P.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 08-OCT-1999; 99US-0158663P.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028301.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 22-FEB-2000; 2000WO-US004414.

XX 24-FEB-2000; 2000WO-US004914.

XX 24-FEB-2000; 2000WO-US005004.

XX 02-MAR-2000; 2000WO-US005841.

XX 15-MAR-2000; 2000WO-US006884.

XX 20-MAR-2000; 2000WO-US007377.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;

WPI; 2001-032160/04.

P-PSDB; AAB65287.

PRO polynucleotides used to produce polypeptides used to target bioactive
molecules such as toxins, radiolabels or antibodies, to specific cells,
to cause targeted cell death.

XX

PS	Claim 2; Fig 303; 935pp; English.	
XX	The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention	
XX		
SQ	Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1630; DB 5; Length 1630;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTGGGTCTTTCATC 60	Db
Db		
QY	61 TTGGATTTGAAGTTGAGAGCAGCATGTTTGGCCACTGAACTCATCTGCTGCCAGTG 120	QY
Db		
QY	121 TTACTGGATTATCTCTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180	QY
Db		
QY	181 CATGTGGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGACAGCAAAATGTATA 240	QY
Db		
QY	241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGACGAATATGTCTATAC 300	QY
Db		
QY	301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCTACACTTGATGGGG 360	QY
Db		
QY	361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420	QY
Db		
QY	421 ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGGCGGTGTTA 480	QY
Db		
QY	481 CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGTTCCATGTGGGTGATTGATTCAG 540	QY
Db		
QY	541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAACACGTCACCAAGGTAGATGATATTT 600	QY
Db		
QY	601 TCAGGACGGCGCGCAAGGAGGAGATTGTTATTCGTTACTACCACAACTCAGGATGTCT 660	QY
Db		
QY	661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAATCTGTGAACCTGTGGGGACATT 720	QY
Db		
QY	721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGGGAGTCAGATGGAGGAACTAC 780	QY

Db	721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGGGAGTCAGATGGAGGAACTAC 780	
QY	781 ACCTGCAGTATCCACCTAGGAACTGGTGTTCAGAAAAACCAATTCGTGCTGATGACG 840	
Db		
Db	781 ACCTGCAGTATCCACCTAGGAACTGGTGTTCAGAAAAACCAATTCGTGCTGATGACG 840	
QY	841 CCGAAGAGCCTCGAACACTGGTGACCCCGGCGAGCCCTGAGGCCCTCTGGTCTTGGGTGGT 900	
Db		
QY	901 AATCAGTTGGTGATCATTTGGGAATTGTCTGTGCCACAATCTCTGCTCTCCCTGTTCTG 960	
Db		
QY	961 AATCAGTTGGTGATCATTTGGGAATTGTCTGTGCCACAATCTCTGCTCTCCCTGTTCTG 960	
QY	961 AATCAGTTGGTGATCATTTGGGAATTGTCTGTGCCACAATCTCTGCTCTCCCTGTTCTG 1020	
Db		
QY	1021 AAGAACACGAAAGACTAATCCAGAGATAAAAGAAAAACCCCTGCCATTTTGAAGATGT 1080	
Db		
QY	1081 GAAGGGGAGAAACACATTTACTCCCCCAATAATTTGTACGGGAGGTGATCGAGGAAAGAA 1140	
Db		
QY	1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200	
Db		
QY	1201 TCAGATCGGAACAACTCACTTGAATAAAAGTCAAGTGGGGAATGCCAAAAACACAGCAA 1260	
Db		
QY	1261 GCCTTTTGAAGAATGGAGATCCCTTTCATCTCAGCAGCGGTGGAGACTCTCTCTCTGTG 1320	
Db		
QY	1321 TGTGTCTGGGCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380	
Db		
QY	1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGACTGGAC 1440	
Db		
QY	1441 AGCTCTGGAGAACAGGCTGTCTGAGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500	
Db		
QY	1501 ACACCTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAAACCCCGCTTGGATCAGACC 1560	
Db		
QY	1561 CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620	
Db		
QY	1621 CCCAATCAA 1630	
Db		
	RESULT 5	
	ABK33633	
	ID ABK33633 standard; cDNA; 1630 BP.	
XX	AC ABK33633;	
XX	DT 08-MAY-2002 (first entry)	
XX	cDNA encoding human PRO protein, Seq ID No 195.	
XX		

KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.

XX Homo sapiens.

PN WO200208288-A2.

PD 31-JAN-2002.

XX 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220585P.

PR 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.

PR 25-JUL-2000; 2000US-0220666P.

PR 26-JUL-2000; 2000US-0220893P.

PR 28-JUL-2000; 2000WO-US020710.

PR 01-AUG-2000; 2000US-0222425P.

PR 22-AUG-2000; 2000US-0227133P.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 28-NOV-2000; 2000US-0253646P.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001WO-US017092.

XX (GETH) GENENTECH INC.

PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

PI WPI; 2002-172001/22.

PI P-PSDB; AAU83689.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,

DR useful for treating a PRO related disorder and for diagnosing tumors such

XX as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor

or liver tumor.

XX Claim 2; Fig 195; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids

CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides

CC encode human secreted proteins. The PRO nucleic acids, polypeptides,

CC agonists and antagonists are useful for treating a PRO related disorder.

CC The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or

CC liver tumour. The PRO polypeptides are useful for stimulating the

CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for

CC stimulating the release of tumour necrosis factor-alpha from human blood,

CC for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular

CC weight markers and for tissue typing. The PRO nucleic acids have

XX applications in molecular biology, including use as hybridisation probes,

XX and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO

XX protein coding sequences of the invention

XX Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

XX SQ

Query Match		100.0%;	Score 1630;	DB 6;	Length 1630;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1630;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTGGTGGTCTCTTCATC	60		
Db	1	CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTGGTGGTCTCTTCATC	60		
QY	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120		
Db	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120		
QY	121	TTACTGGATTATTCCTTGGCCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC	180		
Db	121	TTACTGGATTATTCCTTGGCCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC	180		
QY	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATA	240		
Db	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATA	240		
QY	241	TTCAAGATAGACTGGACTCTGTCAACAGGAGACGCGCAAGGACGAATATGTGCTATAC	300		
Db	241	TTCAAGATAGACTGGACTCTGTCAACAGGAGACGCGCAAGGACGAATATGTGCTATAC	300		
QY	301	TATTACTCCAATCTCAGTGTGCCCTATTTGGCGCTTCCAGAACCGCGTACACTTGTATGGG	360		
Db	301	TATTACTCCAATCTCAGTGTGCCCTATTTGGCGCTTCCAGAACCGCGTACACTTGTATGGG	360		
QY	361	GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA	420		
Db	361	GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA	420		
QY	421	ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA	480		
Db	421	ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA	480		
QY	481	CTGCATGTGCTTCCAGAGGAGGCCCAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAG	540		
Db	481	CTGCATGTGCTTCCAGAGGAGGCCCAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAG	540		
QY	541	ATGGGATGTGTTTCCAGAGCACAGAAAGTGAAACACCTGACCAAGGTAGATGGATATTT	600		
Db	541	ATGGGATGTGTTTCCAGAGCACAGAAAGTGAAACACCTGACCAAGGTAGATGGATATTT	600		
QY	601	TCAGGACGGCGCGCAAGAGGAGATTGTTATTTCTGTTACTACCAAACTCAGGATGTCT	660		
Db	601	TCAGGACGGCGCGCAAGAGGAGATTGTTATTTCTGTTACTACCAAACTCAGGATGTCT	660		
QY	661	GTGGAGTACTCCCAGAGTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT	720		
Db	661	GTGGAGTACTCCCAGAGTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT	720		
QY	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC	780		
Db	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC	780		
QY	781	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAGAAACCATTTGTCTGCATGTCAGC	840		
Db	781	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAGAAACCATTTGTCTGCATGTCAGC	840		
QY	841	CCGGAAGAGCCTCGAACAACCTGGTGACCCCGGACGCCCTGAGGCCCTCTGGTCTTGGTGGT	900		
Db	841	CCGGAAGAGCCTCGAACAACCTGGTGACCCCGGACGCCCTGAGGCCCTCTGGTCTTGGTGGT	900		
QY	901	AATCAGTTGGTGATCATTTGTGGGAATTTGCTGTGCCACAATCCTGCTGCTCCCTGTTCTG	960		
Db	901	AATCAGTTGGTGATCATTTGTGGGAATTTGCTGTGCCACAATCCTGCTGCTCCCTGTTCTG	960		
QY	961	ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG	1020		
Db	961	ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG	1020		
QY	1021	AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCTGCCATTTTGAAGATGT	1080		

Db 1021 AAGACACGAAAGAACTAATCCAGAGATAAAGAAAAACCTGCCATTTTGAAGATGT 1080
QY 1081 GAAGGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 1140
Db 1081 GAAGGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 1140
QY 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200
QY 1201 TCAGATCGGAACAACACTCACTTGAAAAAAGTCAAGTGGGGAATGCCAAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACAACACTCACTTGAAAAAAGTCAAGTGGGGAATGCCAAAAACACAGCAA 1260
QY 1261 GCCTTTTGAGAGAAATGGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
Db 1261 GCCTTTTGAGAGAAATGGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
QY 1321 TGTGTCCTGGGCCACTCTACAGTGATTTCCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
Db 1321 TGTGTCCTGGGCCACTCTACAGTGATTTCCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
QY 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
Db 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGGAACAGGCCTGTGAGGGGAGGAGCATGGACTTGGCCTCTGAGTGGG 1500
Db 1441 AGCTCTGGAGGAACAGGCCTGTGAGGGGAGGAGCATGGACTTGGCCTCTGAGTGGG 1500
QY 1501 AACTGGCCCTGGGAACAGGCCTGTGAGGGGAGGAGCATGGACTTGGCCTCTGAGTGGG 1560
Db 1501 AACTGGCCCTGGGAACAGGCCTGTGAGGGGAGGAGCATGGACTTGGCCTCTGAGTGGG 1560
QY 1561 CTCCTGTGGCAGGGTCTTAGTGATGATGTTACTGGGAAGATCAGAGATAAAACCAA 1620
Db 1561 CTCCTGTGGCAGGGTCTTAGTGATGATGTTACTGGGAAGATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 6
ABL88188
ID ABL88188 standard; cDNA; 1630 BP.
XX ABL88188;
AC ABL88188;
XX 16-MAY-2002 (first entry)
DT Human PRO1387 cDNA sequence SEQ ID NO:233.
XX

Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
gene therapy; cardiovascular disorder; endothelial disorder; cancer;
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
age-related macular degeneration; arterial restenosis; angina;
rheumatoid arthritis; myocardial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.
XX
XX WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-021956P.

PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.
P-PSDB; ABB84933.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.

Claim 2; Fig 233; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCCTCCCTGGGTCTTCATC 60
Db 1 CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCCTCCCTGGGTCTTCATC 60

QY 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCCTGCTGCCAGTG 120
Db 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCCTGCTGCCAGTG 120
QY 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
Db 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
QY 181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGCAAAATGTATA 240
Db 181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGCAAAATGTATA 240
QY 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGACGAATATGTCTATAC 300
Db 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGACGAATATGTCTATAC 300
QY 301 TATTACTCCAATCTCAGTGTGCCCTTATTTGGGCGCTTCCAGAACCGCGTACACTTGTATGGG 360
Db 301 TATTACTCCAATCTCAGTGTGCCCTTATTTGGGCGCTTCCAGAACCGCGTACACTTGTATGGG 360
QY 361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA 420
Db 361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA 420
QY 421 ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTTA 480
Db 421 ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTTA 480
QY 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTTCCATGCTGATGTTGATTCAG 540
Db 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTTCCATGCTGATGTTGATTCAG 540
QY 541 ATGGGATGTGTTTCCAGAGCAGCAGAGTGAAACACTGACCAAGGTAGAAATGATATT 600
Db 541 ATGGGATGTGTTTCCAGAGCAGCAGAGTGAAACACTGACCAAGGTAGAAATGATATT 600
QY 601 TCAGGACGGCGCGCAAGAGGAGATTGTTATTTCTGTTACTACCAAACTCAGGATGCT 660
Db 601 TCAGGACGGCGCGCAAGAGGAGATTGTTATTTCTGTTACTACCAAACTCAGGATGCT 660
QY 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAACTCGTGTGAACTCGTGGGGACATT 720
Db 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAACTCGTGTGAACTCGTGGGGACATT 720
QY 721 TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAACTAC 780
Db 721 TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAACTAC 780
QY 781 ACCTGCAGTATCCACCTAGGGAACCTGTTTCAAGAAACCAATTTGCTGTCATGTCAGC 840
Db 781 ACCTGCAGTATCCACCTAGGGAACCTGTTTCAAGAAACCAATTTGCTGTCATGTCAGC 840
QY 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCGCTCTGGTCTTGGTGGT 900
Db 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCGCTCTGGTCTTGGTGGT 900
QY 901 AATCAGTTGGTGATCAATTTGGGAAATTTGTTGTCGCCACAACTCTGCTCCCTGTTCTG 960
Db 901 AATCAGTTGGTGATCAATTTGGGAAATTTGTTGTCGCCACAACTCTGCTCCCTGTTCTG 960
QY 961 ATATTGATCGTGAAGAAGACCTGTGGAATTAAGAGTTTCAAGTCTTACAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAAGACCTGTGGAATTAAGAGTTTCAAGTCTTACAGTCTTGGTG 1020
QY 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCACTGCAATTTTGAAGATGT 1080
Db 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCACTGCAATTTTGAAGATGT 1080
QY 1081 GAAGGGGAGAAACACATTTACTCCCAATAATGTACGGGAGGTGATCGAGGAAGAAGAA 1140
Db 1081 GAAGGGGAGAAACACATTTACTCCCAATAATGTACGGGAGGTGATCGAGGAAGAAGAA 1140

QY 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG 1200
QY 1201 TCAGATCGGAACAACACTCACTTGAATAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACAACACTCACTTGAATAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA 1260
QY 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCTATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
Db 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCTATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
QY 1321 TGTGTCTGGGCCACTCTACCAAGTATTTTCAAGTCCCGCTCTCCAGCTGTCTCCTCTGT 1380
Db 1321 TGTGTCTGGGCCACTCTACCAAGTATTTTCAAGTCCCGCTCTCCAGCTGTCTCCTCTGT 1380
QY 1381 CTCATTGTTTGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
Db 1381 CTCATTGTTTGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGAACAGGCCCTGCTGAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
Db 1441 AGCTCTGGAGAACAGGCCCTGCTGAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
QY 1501 AACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAAACCCCGCTTGGATCAGACC 1560
Db 1501 AACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAAACCCCGCTTGGATCAGACC 1560
QY 1561 CTCTGTGGGACAGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA 1620
Db 1561 CTCTGTGGGACAGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 7
ABL95677

ID ABL95677 standard; cDNA; 1630 BP.

XX ABL95677;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO1387 SEQ ID NO: 233.

DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US02328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030973.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX

PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX

DR WPI; 2002-171999/22.
DR P-PSDB; ABB95539.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 1; Fig 233; 567pp; English.

XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX

SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCTCAGTGCAGCTGTGGGGAGATTTCAGTGCATTCGCTCCCTGGGTCTCTTCATC 60
Db 1 CGGCTCAGTGCAGCTGTGGGGAGATTTCAGTGCATTCGCTCCCTGGGTCTCTTCATC 60
Qy 61 TTGGATTTGAAAGTTGAGACGAGCATGTTTGGCCCACTGAAACTCATCTCTGCTGCCAGTG 120

Db 61 TTGGATTTGAAAGTTGAGACGAGCATGTTTGGCCCACTGAAACTCATCTCTGCTGCCAGTG 120
Qy 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
Db 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
Qy 181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAACAAATGTATA 240
Db 181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAACAAATGTATA 240
Qy 241 TTCAAGATAGACTGGAATCTGTCAACAGGAGAGCAGCCCAAGGACGAATATGTCTATAC 300
Db 241 TTCAAGATAGACTGGAATCTGTCAACAGGAGAGCAGCCCAAGGACGAATATGTCTATAC 300
Qy 301 TATTACTCCAATCTCAGTGTGCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGG 360
Db 301 TATTACTCCAATCTCAGTGTGCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGG 360
Qy 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACAGGGA 420
Db 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACAGGGA 420
Qy 421 ACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA 480
Db 421 ACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA 480
Qy 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTCATGTTGGGTGATTCAGTTCAG 540
Db 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTCATGTTGGGTGATTCAGTTCAG 540
Qy 541 ATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACACGTGACCAAGGTAGATTCGATATT 600
Db 541 ATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACACGTGACCAAGGTAGATTCGATATT 600
Qy 601 TCAGGACGGCGCAAGAGGAGAGATTGTAATTCGTTACTACCAAACTCAGGATGTCT 660
Db 601 TCAGGACGGCGCAAGAGGAGAGATTGTAATTCGTTACTACCAAACTCAGGATGTCT 660
Qy 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTTGGGGACATT 720
Db 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTTGGGGACATT 720
Qy 721 TTCCGCAATGACGGTTCCATCATGTTCAAGGAGTGAGGAGTCCAGATGGAGAAACTAC 780
Db 721 TTCCGCAATGACGGTTCCATCATGTTCAAGGAGTGAGGAGTCCAGATGGAGAAACTAC 780
Qy 781 ACCTGAGTATCCACCTAGGAACTGTTGTTCAAGAAACCAATTCGTCATGTCCAGC 840
Db 781 ACCTGAGTATCCACCTAGGAACTGTTGTTCAAGAAACCAATTCGTCATGTCCAGC 840
Qy 841 CCGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCCCTCTGGTCTTGGGTGGT 900
Db 841 CCGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCCCTCTGGTCTTGGGTGGT 900
Qy 901 AATCAGTTGGTGATCATTTGTGGGAATTCGTGTGCCACAATCCTGCTGCTCCCTGTTCTG 960
Db 901 AATCAGTTGGTGATCATTTGTGGGAATTCGTGTGCCACAATCCTGCTGCTCCCTGTTCTG 960
Qy 961 ATATTGATCGTGAAGAGACCTGTGGAATAAGAGTTTCAGTGAATTCACAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAGACCTGTGGAATAAGAGTTTCAGTGAATTCACAGTCTTGGTG 1020
Qy 1021 AAGAACAAGAGAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT 1080
Db 1021 AAGAACAAGAGAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT 1080
Qy 1081 GAAGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAGAA 1140
Db 1081 GAAGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAGAA 1140
Qy 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCCAGTTCGAGGCTTCTCTGAGG 1200

Db	1141	CCAAAGTGAAAAATCAGAGGCCACCTACATGACCCAGTTTGGCCTTCTCTGAGG	1200
QY	1201	TCAGATCGGAACAACACTCATTGAAAAAAGTCAAGTGGGGAATGCCAAAAACACAGCAA	1260
Db	1201	TCAGATCGGAACAACACTCATTGAAAAAAGTCAAGTGGGGAATGCCAAAAACACAGCAA	1260
QY	1261	GCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG	1320
Db	1261	GCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG	1320
QY	1321	TGTGTCCTGGGCCACTCTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCCTGT	1380
Db	1321	TGTGTCCTGGGCCACTCTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCCTGT	1380
QY	1381	CTCATTTGTTTGGTCAATACACTGAAGATGGAGATTTGGAGCCTGGCAGAGAGACTGGAC	1440
Db	1381	CTCATTTGTTTGGTCAATACACTGAAGATGGAGATTTGGAGCCTGGCAGAGAGACTGGAC	1440
QY	1441	AGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG	1500
Db	1441	AGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG	1500
QY	1501	ACACTGGCCCTGGGAACCAAGCTGAGTGGCTGAGTGGCCTCAAAACCCCGTTGGATCAGACC	1560
Db	1501	ACACTGGCCCTGGGAACCAAGCTGAGTGGCTGAGTGGCCTCAAAACCCCGTTGGATCAGACC	1560
QY	1561	CTCCTGTGGGCGAGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA	1620
Db	1561	CTCCTGTGGGCGAGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA	1620
QY	1621	CCCAAAATCAA 1630	
Db	1621	CCCAAAATCAA 1630	

RESULT 8
ABX77981
ID ABX77981 standard; cDNA; 1630 BP.
XX
AC ABX77981;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polynucleotide #134.
XX
KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
EN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.

PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088026P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088030P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088734P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088742P.
PR	10-JUN-1998;	98US-0088810P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088858P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089440P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089532P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089599P.
PR	17-JUN-1998;	98US-0089600P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089801P.
PR	18-JUN-1998;	98US-0089907P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089947P.
PR	19-JUN-1998;	98US-0089948P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	23-JUN-1998;	98US-0090349P.
PR	23-JUN-1998;	98US-0090355P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090431P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
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PR	24-JUN-1998;	98US-0090472P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	24-JUN-1998;	98US-0090542P.
PR	24-JUN-1998;	98US-0090557P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	01-JUL-1998;	98US-0091360P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091519P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091633P.
PR	02-JUL-1998;	98US-0091646P.
PR	02-JUL-1998;	98US-0091673P.
PR	07-JUL-1998;	98US-0091978P.
PR	07-JUL-1998;	98US-0091982P.
PR	09-JUL-1998;	98US-0092182P.
PR	10-JUL-1998;	98US-0092472P.

Db 721 TTCCGAATGACGGTTCCATCATGTTCAAGGAGTGAGGAGTCAGATGGAGGAACACTAC 780

QY 781 ACCTGCAGTATCCACTAGGGAACCTGGTGTTCAGAAAAACCAATTGTGCTGCATGTCAGC 840

Db 781 ACCTGCAGTATCCACTAGGGAACCTGGTGTTCAGAAAAACCAATTGTGCTGCATGTCAGC 840

QY 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTTGGTGGT 900

Db 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTTGGTGGT 900

QY 901 AATCAGTTGGTGATCATTTGTGGGAATTGTGTGCCACAATCCTGTGCTCCCTGTTCTG 960

Db 901 AATCAGTTGGTGATCATTTGTGGGAATTGTGTGCCACAATCCTGTGCTCCCTGTTCTG 960

QY 961 ATATTGATCGTGAAGAGACCTGTGGAAATAAGAGTTTCAGTGAATTTACAGTCTTTGGTG 1020

Db 961 ATATTGATCGTGAAGAGACCTGTGGAAATAAGAGTTTCAGTGAATTTACAGTCTTTGGTG 1020

QY 1021 AAGAACGGAAGAGACTAATCCAGAGATAAAAGAAACCCCTGCCATTTTGAAGATGT 1080

Db 1021 AAGAACGGAAGAGACTAATCCAGAGATAAAAGAAACCCCTGCCATTTTGAAGATGT 1080

QY 1081 GAAGGGGAGAAACACATTTACTCCCCCAATAATTGTACGGAGGTGATCCAGGAAGAAGAA 1140

Db 1081 GAAGGGGAGAAACACATTTACTCCCCCAATAATTGTACGGAGGTGATCCAGGAAGAAGAA 1140

QY 1141 CCAAGTGAATAATCAGAGGCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG 1200

Db 1141 CCAAGTGAATAATCAGAGGCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG 1200

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Db 1201 TCAGATCGGAACAACACTCACTTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAA 1260

QY 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGTGGAGACTCTCTCCTGTG 1320

Db 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGTGGAGACTCTCTCCTGTG 1320

QY 1321 TGTGTCCTGGCCACTCTACAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT 1380

Db 1321 TGTGTCCTGGCCACTCTACAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT 1380

QY 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGGCAGAGAGACTGGAC 1440

Db 1381 CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGGCAGAGAGACTGGAC 1440

QY 1441 AGCTCTGGAGAACAGGCCTGTGAGGGGAGGGAGCATGGACTTGGCCTCTGAGTGGG 1500

Db 1441 AGCTCTGGAGAACAGGCCTGTGAGGGGAGGGAGCATGGACTTGGCCTCTGAGTGGG 1500

QY 1501 ACACCTGGCCCTGGGAACCCAGGCTGAGCTGAGTGGCCTCAAACCCCGCTTGGATCAGACC 1560

Db 1501 ACACCTGGCCCTGGGAACCCAGGCTGAGCTGAGTGGCCTCAAACCCCGCTTGGATCAGACC 1560

QY 1561 CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA 1620

Db 1561 CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA 1620

QY 1621 CCCAAATCAA 1630

Db 1621 CCCAAATCAA 1630

RESULT 9

ABX80393
ID ABX80393 standard; DNA; 1630 BP.

XX AC ABX80393;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO1384 DNA.

XX

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

XX Homo sapiens.

OS US2002132252-A1.

XX 19-SEP-2002.

PN 14-NOV-2001; 2001US-00990442.

XX 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

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PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

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PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088858P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089440P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 16-JUN-1998; 98US-0089532P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089599P.

PR 17-JUN-1998; 98US-0089600P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

DR WPI; 2003-247083/24.
DR P-PSDB; ABU59181.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.

PS Claim 2; Fig 305; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating conditions or disorders where angiogenesis would be
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,

CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide

XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTGGTGTCTTCATC 60
Db |||||
QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTGGTGTCTTCATC 60
Db |||||
QY 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG 120
Db |||||
QY 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG 120
Db |||||
QY 121 TTACTGGATTATTCCTTGGGCTGAATGACCTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
Db |||||
QY 121 TTACTGGATTATTCCTTGGGCTGAATGACCTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
Db |||||
QY 181 CATGTGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGCAAAATGTATA 240
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QY 181 CATGTGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGCAAAATGTATA 240
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QY 241 TTCAAGATAGACTGGACTCTGTCTCAGGAGAGCAGCCCAAGAGGATATGTGTATAC 300
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QY 241 TTCAAGATAGACTGGACTCTGTCTCAGGAGAGCAGCCCAAGAGGATATGTGTATAC 300
Db |||||
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Db |||||
QY 301 TATTACTCCAAATCTCAGTGTGCTATTGGGCGCTTCCAGAACCCGCTACACTTGATGGG 360
Db |||||
QY 361 GACATCTTATGCAATGATGGCTCTCTCTCTCCTCCTCAAGATGTGCAAGAGGCTGACCCAGGGA 420
Db |||||
QY 361 GACATCTTATGCAATGATGGCTCTCTCTCTCCTCCTCAAGATGTGCAAGAGGCTGACCCAGGGA 420
Db |||||
QY 421 ACCTATATCTGTGAAATCCGCTCAAAGGGAGAGCCAGGTGTTTCAAGAGGCGGTGTA 480
Db |||||
QY 421 ACCTATATCTGTGAAATCCGCTCAAAGGGAGAGCCAGGTGTTTCAAGAGGCGGTGTA 480
Db |||||
QY 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGGCTCATGGTCCATGTGGTGGATTGATTCAG 540
Db |||||
QY 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGGCTCATGGTCCATGTGGTGGATTGATTCAG 540
Db |||||
QY 541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAATTT 600
Db |||||
QY 541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAATTT 600
Db |||||
QY 601 TCAGGACGGCGCGCAAGAGGAGAGATTGTTATTTTCGTTTACTACCAAACTCAGGATGTCT 660
Db |||||
QY 601 TCAGGACGGCGCGCAAGAGGAGAGATTGTTATTTTCGTTTACTACCAAACTCAGGATGTCT 660
Db |||||
QY 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
Db |||||
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Db |||||
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Db |||||
QY 721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTGAGGAGTAACTAC 780
Db |||||

Qy 781 ACCTGAGTATCCACCTAGGGAACCTGGTGTTCAGAAAAACCAATTGTGCTGCATGTCAGC 840
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781 ACCTGAGTATCCACCTAGGGAACCTGGTGTTCAGAAAAACCAATTGTGCTGCATGTCAGC 840
Qy 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTTGGGTGT 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTTGGGTGT 900
Qy 901 AATCAGTTGGTGATCAATTGTGGGAATTGTGTGCCAATCCTGCTGCTCCCTGTTCTG 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 AATCAGTTGGTGATCAATTGTGGGAATTGTGTGCCAATCCTGCTGCTCCCTGTTCTG 960
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RESULT 10

ACA69299
ID ACA69299 standard; cDNA; 1630 BP.

XX ACA69299;

AC

XX 26-JUN-2003 (first entry)

DT

XX Human cDNA encoding secreted/transmembrane protein PRO1387.

DE

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;

KW cardiac insufficiency disorders; angiogenesis; wound healing;

KW

KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.
XX Homo sapiens.
OS
XX US2003032023-A1.
PN
XX 13-FEB-2003.
PD
XX 14-NOV-2001; 2001US-00990711.
PF
XX 16-JUN-1997; 97US-0049787P.
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RESULT 11
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AC ACD24112;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1387 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
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PD 13-FEB-2003.
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PF 06-MAY-2002; 2002US-00140474.
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PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
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PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341980/32.
DR P-PSDB; ABO17875.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, axquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 2; Fig 519; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTGCCTCCCTGGGTGCTTCATC 60
Db |||||
QY 61 TTGGATTGAAAAGTTGAGAGCAGCATGTTTTCCTCCACTGAACTCATCTGCTGCCAGTG 120
Db |||||
QY 61 TTGGATTGAAAAGTTGAGAGCAGCATGTTTTCCTCCACTGAACTCATCTGCTGCCAGTG 120
Db |||||
QY 121 TTTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
Db |||||
QY 121 TTTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
Db |||||
QY 181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGCAAGCAATGTATA 240
Db |||||
QY 181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGCAAGCAATGTATA 240
Db |||||
QY 241 TTCAAGATAGACTGGACTCTGTACCAGGAGCAGCCAGGACGAATATGTGCTATAC 300
Db |||||
QY 241 TTCAAGATAGACTGGACTCTGTACCAGGAGCAGCCAGGACGAATATGTGCTATAC 300
Db |||||
QY 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCGCTACATTGATGGG 360
Db |||||
QY 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCGCTACATTGATGGG 360
Db |||||
QY 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCCAGGGA 420
Db |||||
QY 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCCAGGGA 420
Db |||||
QY 421 ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAGGCGGTGGTA 480

Db 421 ACCTATATCTGTGAATCCGCCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA 480
Qy 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTTCCATGTGGTGGATTGATTGAG 540
Db 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTTCCATGTGGTGGATTGATTGAG 540
Qy 541 ATGGGATGTGTTTTCCAGAGCACAGAACTGAAACACGTCACCAAGGTAGAAATGGATATTT 600
Db 541 ATGGGATGTGTTTTCCAGAGCACAGAACTGAAACACGTCACCAAGGTAGAAATGGATATTT 600
Qy 601 TCAGGACGGCGCGCAAGAGGAGATTGTTATTTTCGTTACTACCAAACTCAGGATGTCT 660
Db 601 TCAGGACGGCGCGCAAGAGGAGATTGTTATTTTCGTTACTACCAAACTCAGGATGTCT 660
Qy 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTGGGGGACATT 720
Db 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTGGGGGACATT 720
Qy 721 TTCCGCAATGACGGTTCCCATCATGCTTCAAGGAGTGAGGAGTCAGATGAGGAAACTAC 780
Db 721 TTCCGCAATGACGGTTCCCATCATGCTTCAAGGAGTGAGGAGTCAGATGAGGAAACTAC 780
Qy 781 ACCTGCAGTATCCACCTAGGAAACCTGGTGTTCAGAAACCAATTGTGTGTCATGTCAGC 840
Db 781 ACCTGCAGTATCCACCTAGGAAACCTGGTGTTCAGAAACCAATTGTGTGTCATGTCAGC 840
Qy 841 CCGGAAGAGCCTCGAAACACTGGTGACCCCGCAGCCCTGAGGCCTCTGGTCTTGGTGGT 900
Db 841 CCGGAAGAGCCTCGAAACACTGGTGACCCCGCAGCCCTGAGGCCTCTGGTCTTGGTGGT 900
Qy 901 AATCAGTTGGTGATCATTTGTGGGAATTGTGTGTGCCACAATCTGCTGCCCTGTTCTG 960
Db 901 AATCAGTTGGTGATCATTTGTGGGAATTGTGTGTGCCACAATCTGCTGCCCTGTTCTG 960
Qy 961 ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTTCAGTGAATTCACAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTTCAGTGAATTCACAGTCTTGGTG 1020
Qy 1021 AAGAACACGAAAGAACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
Db 1021 AAGAACACGAAAGAACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
Qy 1081 GAAGGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA 1140
Db 1081 GAAGGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA 1140
Qy 1141 CCAAGTGAAATAATCAGAGGCCACTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAATAATCAGAGGCCACTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGG 1200
Qy 1201 TCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGGGATGCCAAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGGGATGCCAAAAACACAGCAA 1260
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Db 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCAATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
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Db 1321 TGTGTCTGGGCCACTCTACAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT 1380
Qy 1381 CTCATTGTTTGTGTCATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
Db 1381 CTCATTGTTTGTGTCATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
Qy 1441 AGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
Db 1441 AGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
Qy 1501 AACTGGCCCTGGGAACCAAGGCTGAGTGAGTGCCTCAACCCCGCTTGGATCAGACC 1560

Db 1501 AACTGGCCCTGGGAACCAGGCTGAGTGAGTGGCCTCAAAACCCCGCTTGGATCAGACC 1560
Qy 1561 CTCTGTGGGCAGGGTCTTAGTGATGAGTTACTCGGAAGAATCAGAGATAAAACCAA 1620
Db 1561 CTCTGTGGGCAGGGTCTTAGTGATGAGTTACTCGGAAGAATCAGAGATAAAACCAA 1620
Qy 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630
RESULT 12
ABX90370
ID ABX90370 standard; cDNA; 1630 BP.
XX
AC ABX90370;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein cDNA, #170.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; therapeutic; gene therapy.
OS Homo sapiens.
XX
PN US2002160384-A1.
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992599.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.

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PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089533P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089539P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US006884.
PR 02-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR P-PSDB; ABU60611.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 2; Fig 303; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
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CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABX90083-ABX90468 are the
CC genes encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 1630; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCCTCCCTGGGTGCTCTTCATC 60
Db 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCCTCCCTGGGTGCTCTTCATC 60
QY 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCCTGCTGCCAGTG 120
Db 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCCTGCTGCCAGTG 120
QY 121 TTTACTGGATTATTCCTTGGGCTTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
Db 121 TTTACTGGATTATTCCTTGGGCTTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
QY 181 CATGTGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAACAAATGTATA 240
Db 181 CATGTGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAACAAATGTATA 240
QY 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGAGGAATATGTGCTATAC 300
Db 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGGAGGAATATGTGCTATAC 300
QY 301 TATTACTCCAATCTCAGTGTGCCTTATTTGGCGCTTCCAGAACCCGCTACACTTGTATGGG 360
Db 301 TATTACTCCAATCTCAGTGTGCCTTATTTGGCGCTTCCAGAACCCGCTACACTTGTATGGG 360
QY 361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420
Db 361 GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420
QY 421 ACCTATATCTGTGAAATCCGCTTCAAAGGGGAGAGCCAGGTGTTCAGAGGCGGTGTA 480
Db 421 ACCTATATCTGTGAAATCCGCTTCAAAGGGGAGAGCCAGGTGTTCAGAGGCGGTGTA 480
QY 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTTCATGTCATGTGGGTGGATTGATTCAG 540
Db 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTTCATGTCATGTGGGTGGATTGATTCAG 540
QY 541 ATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACCGTGACCAAGGTAGATGGATATT 600
Db 541 ATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACCGTGACCAAGGTAGATGGATATT 600
QY 601 TCAGGACGGCGCCAAAGGAGGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCT 660
Db 601 TCAGGACGGCGCCAAAGGAGGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCT 660
QY 661 GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
Db 661 GTGGAGTACTCCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
QY 721 TTCCGCAATGACGGTTCATCATGCTTCAAGAGTGAGGAGTGAGGAGTCAAGTGGAGAACTAC 780
Db 721 TTCCGCAATGACGGTTCATCATGCTTCAAGAGTGAGGAGTGAGGAGTCAAGTGGAGAACTAC 780
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QY	781	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAACCAATTGTGCTGCATGTCAGC	840	KW	anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
Db	781	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAACCAATTGTGCTGCATGTCAGC	840	KW	gene; ss.
QY	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT	900	OS	Homo sapiens.
Db	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT	900	XX	
QY	901	AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCCTGCTGCCCTGTTCTG	960	PN	US2003036635-A1.
Db	901	AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCCTGCTGCCCTGTTCTG	960	XX	20-FEB-2003.
QY	961	ATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAAGTTCAGTGAATTCACAGTCTTGGTG	1020	XX	28-AUG-2002; 2002US-00230163.
Db	961	ATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAAGTTCAGTGAATTCACAGTCTTGGTG	1020	PF	25-JUL-2000; 2000US-0220638P.
QY	1021	AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAAGATGT	1080	PR	01-JUN-2001; 2001WO-US017800.
Db	1021	AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAAGATGT	1080	PR	29-JUN-2001; 2001WO-US021066.
QY	1081	GAAGGGGAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAAGAAGAA	1140	PR	09-APR-2002; 2002US-00119480.
Db	1081	GAAGGGGAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAAGAAGAA	1140	XX	(GETH) GENENTECH INC.
QY	1141	CCAAGTGAATAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCCTTCTCTGAGG	1200	XX	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
Db	1141	CCAAGTGAATAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCCTTCTCTGAGG	1200	PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
QY	1201	TCAGATCGGAACAACACTCATTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA	1260	XX	WPI; 2003-342045/32.
Db	1201	TCAGATCGGAACAACACTCATTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA	1260	DR	P-PSDB; ABU80836.
QY	1261	GCCTTTTGAGAAGAAATGGAGAGTCCCTTCATCTCAGACGCGTGGAGACTCTCTCCTGTG	1320	PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,
Db	1261	GCCTTTTGAGAAGAAATGGAGAGTCCCTTCATCTCAGACGCGTGGAGACTCTCTCCTGTG	1320	PT	useful for the manufacture of a medicament for diagnosing or treating
QY	1321	TGTGTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT	1380	XX	tumor.
Db	1321	TGTGTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCCTCTGT	1380	PS	Claim 2; Fig 195; 314pp; English.
QY	1381	CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC	1440	XX	The present invention relates to the isolation of novel human PRO
Db	1381	CTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC	1440	CC	polypeptides, and the polynucleotide sequences encoding them. The PRO
QY	1441	AGCTCTGGAGGAACAGGCCCTGTGAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGGG	1500	CC	polypeptides are secreted and transmembrane proteins. The PRO
Db	1441	AGCTCTGGAGGAACAGGCCCTGTGAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGGG	1500	CC	polypeptides and polynucleotides are useful for preparing a medicament
QY	1501	ACACTGGCCCTGGGAACCAAGCTGAGTGGCCCTCAACCCCGCTTGGATCAGAAC	1560	CC	useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
Db	1501	ACACTGGCCCTGGGAACCAAGCTGAGTGGCCCTCAACCCCGCTTGGATCAGAAC	1560	CC	specific cells, tissues or serum, and for affinity purification of PRO
QY	1561	CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA	1620	CC	from recombinant cell culture or natural sources. ACA66841-ACA66962
Db	1561	CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA	1620	CC	represent cDNA sequences encoding the human PRO polypeptides of the
QY	1621	CCCAAAATCAA 1630		CC	invention. Note: The sequence data for this patent was obtained in
Db	1621	CCCAAAATCAA 1630		CC	electronic format directly from the USPTO web site at
RESULT 13				CC	seqdata.uspto.gov/psipsDIDEntry.html
ACA66938				XX	Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;
ID	ACA66938 standard; cDNA; 1630 BP.			Query Match	100.0%; Score 1630; DB 7; Length 1630;
XX				Best Local Similarity	100.0%; Pred. No. 0;
AC				Matches 1630; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX				QY	1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTTGCCCTCCCTGGTGTCTTCATC
XX				Db	1 CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTTGCCCTCCCTGGTGTCTTCATC
XX				QY	61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCTGCTGCCAGTG
XX				Db	61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCTGCTGCCAGTG
XX				QY	121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC
XX				Db	121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC
XX				QY	181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGACAGAACAAATGTATA
XX				Db	181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGACAGAACAAATGTATA
XX				QY	241 TTCAAGATAGACTGGACTCTGTACCAGGAGACACGCCAAGACGAATATGTCTATAC
XX				Db	241 TTCAAGATAGACTGGACTCTGTACCAGGAGACACGCCAAGACGAATATGTCTATAC
XX				QY	301 TATTACTCCAATCTCAGTGTGCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGG
XX				Db	301 TATTACTCCAATCTCAGTGTGCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGG
DE	cdNA encoding human PRO polypeptide #98.				
XX	Human; PRO polypeptide; secreted and transmembrane protein;				

QY 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGTGCAAGAGCTGACCAAGGA 420
Db |||||
361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGTGCAAGAGCTGACCAAGGA 420
QY 421 ACCTATATCTGTGAATCCGCCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTTA 480
Db |||||
421 ACCTATATCTGTGAATCCGCCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTTA 480
QY 481 CTGCATGTGCTTCCAGAGGAGCCCCAAAGAGCTCATGTGCCATGTGGGTGGATTGATTCAG 540
Db |||||
481 CTGCATGTGCTTCCAGAGGAGCCCCAAAGAGCTCATGTGCCATGTGGGTGGATTGATTCAG 540
QY 541 ATGGGATGTGTTTTCCAGAGCACAGAACTGAAACACGTGACCAAGGTAGATGATATTT 600
Db |||||
541 ATGGGATGTGTTTTCCAGAGCACAGAACTGAAACACGTGACCAAGGTAGATGATATTT 600
QY 601 TCAGGACGGCGCGCAAGAGGAGATTGTATTTCTGTTACTACCAAACTCAGGATGTCT 660
Db |||||
601 TCAGGACGGCGCGCAAGAGGAGATTGTATTTCTGTTACTACCAAACTCAGGATGTCT 660
QY 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACTGTGGGGGACATT 720
Db |||||
661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACTGTGGGGGACATT 720
QY 721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGAACTAC 780
Db |||||
721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGAACTAC 780
QY 781 ACCTGAGTATCCACCTAGGGAACTGTGGTGTTCAGAGAAACCATTTGCTGCAATGTCAGC 840
Db |||||
781 ACCTGAGTATCCACCTAGGGAACTGTGGTGTTCAGAGAAACCATTTGCTGCAATGTCAGC 840
QY 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCCCTCTGGTCTTTGGGTGGT 900
Db |||||
841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCCCTCTGGTCTTTGGGTGGT 900
QY 901 AATCAGTTGGTGATCAATTGTGGGAATGTCTGTGCCAATCTGTGCTCCCTGTTCTG 960
Db |||||
901 AATCAGTTGGTGATCAATTGTGGGAATGTCTGTGCCAATCTGTGCTCCCTGTTCTG 960
QY 961 ATATTGATCGTGAAGAACCTGTGGAATAAGAGTTTCAAGTTCAGTGAATTTACAGTCTTGGTG 1020
Db |||||
961 ATATTGATCGTGAAGAACCTGTGGAATAAGAGTTTCAAGTTCAGTGAATTTACAGTCTTGGTG 1020
QY 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAGAAACCCCTGCCATTTTGAAGATGT 1080
Db |||||
1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAGAAACCCCTGCCATTTTGAAGATGT 1080
QY 1081 GAAGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 1140
Db |||||
1081 GAAGGGAGAAACACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAA 1140
QY 1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCCAGTTCCTGCTTCTCTGAGG 1200
Db |||||
1141 CCAAGTGAAAAATCAGAGGCCACCTACATGACCCAGTTCCTGCTTCTCTGAGG 1200
QY 1201 TCAGATCGGAACAACTCACTTGAAAAAAGTCAAGTGGGGGAAATGCCAAAAACACAGCAA 1260
Db |||||
1201 TCAGATCGGAACAACTCACTTGAAAAAAGTCAAGTGGGGGAAATGCCAAAAACACAGCAA 1260
QY 1261 GCCTTTTGAGAAGATGGAGATCCCTTCTATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
Db |||||
1261 GCCTTTTGAGAAGATGGAGATCCCTTCTATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
QY 1321 TGTGCTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
Db |||||
1321 TGTGCTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
QY 1381 CTCAATGTTTGGTCAATACACTGAAGATGGAGATTTGGAGCCTGCGAGAGACTGGAC 1440
Db |||||
1381 CTCAATGTTTGGTCAATACACTGAAGATGGAGATTTGGAGCCTGCGAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGGAACAGGCCTGTCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500

Db 1441 AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGG 1500
QY 1501 ACACCTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCCTCAAAACCCCGTTGGATCAGACC 1560
Db |||||
1501 ACACCTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCCTCAAAACCCCGTTGGATCAGACC 1560
QY 1561 CTCCTGTGGCAGGGTCTTCTAGTGGATGATTACTGGGAAGAATCAGAGATAAAACCAA 1620
Db |||||
1561 CTCCTGTGGCAGGGTCTTCTAGTGGATGATTACTGGGAAGAATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db |||||
1621 CCCAAATCAA 1630

RESULT 14
ACD68690
ID ACD68690 standard; cDNA; 1630 BP.
XX
AC ACD68690;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1387 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cytosstatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioindicator; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
XX
DR P-PSDB; ABO33802.
XX
PT New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
XX wounds in a mammal.
PS Claim 2; Fig 195; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioeffectors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte

cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 7; Length 1630;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCTCGAGTCAGCTGTGGGAGATTTCAGTGCATTTCCCTCCCTGGTGCTCTTCATC 60
Dbb 1 CGGCTCGAGTCAGCTGTGGGAGATTTCAGTGCATTTCCCTCCCTGGTGCTCTTCATC 60
Qy 61 TTGGATTTGAAAGTTGAGACAGCATGTTTGGCCACTGAACTCATCCCTGCCAGTG 120
Dbb 61 TTGGATTTGAAAGTTGAGACAGCATGTTTGGCCACTGAACTCATCCCTGCCAGTG 120
Qy 121 TTAGTGATTTGAAAGTTGAGACAGCATGTTTGGCCACTGAACTCATCCCTGCCAGTG 180
Dbb 121 TTAGTGATTTGAAAGTTGAGACAGCATGTTTGGCCACTGAACTCATCCCTGCCAGTG 180
Qy 181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTCCAGAGACAGAAATGTATA 240
Dbb 181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTCCAGAGACAGAAATGTATA 240
Qy 241 TTCAAGATAGACTGGACTCTGTCCAGGAGACGCGCAAGGACGAATATGTCTATAC 300
Dbb 241 TTCAAGATAGACTGGACTCTGTCCAGGAGACGCGCAAGGACGAATATGTCTATAC 300
Qy 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTGATGGG 360
Dbb 301 TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTGATGGG 360
Qy 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGA 420
Dbb 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGA 420
Qy 421 ACCTATATCTGTGAAATCCGCTCAAAAGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA 480
Dbb 421 ACCTATATCTGTGAAATCCGCTCAAAAGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA 480
Qy 481 CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGGTCCATGTGGGTGATGATTCAG 540
Dbb 481 CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGGTCCATGTGGGTGATGATTCAG 540
Qy 541 ATGGGATGTGTTTCCAGAGACAGAAAGTGAACACGTCAGCAAGGTAGATGATATT 600
Dbb 541 ATGGGATGTGTTTCCAGAGACAGAAAGTGAACACGTCAGCAAGGTAGATGATATT 600
Qy 601 TCAGGACGGCGCGCAAGAGGAGATGTAATTCGTTACTACCAAACTCAGGATGTCT 660
Dbb 601 TCAGGACGGCGCGCAAGAGGAGATGTAATTCGTTACTACCAAACTCAGGATGTCT 660
Qy 661 GTGGAGTACTCCAGAGCTGGGCGCACTTCCAGAATCGTGTGAACCTGGTGGGGACATT 720
Dbb 661 GTGGAGTACTCCAGAGCTGGGCGCACTTCCAGAATCGTGTGAACCTGGTGGGGACATT 720
Qy 721 TTCCGCAATGACGGTTCCATCATGCTTCAAGAGTGAGGGAGTCAGATGGAGAAACTAC 780
Dbb 721 TTCCGCAATGACGGTTCCATCATGCTTCAAGAGTGAGGGAGTCAGATGGAGAAACTAC 780
Qy 781 ACCTGCAGTATCCACCTAGGGAACCTGGTGTCAAGAAACCATTGTGCTGCATGTCAGC 840

Dbb 781 ACCTGCAGTATCCACCTAGGGAACCTGGTGTCAAGAAACCATTGTGCTGCATGTCAGC 840
Qy 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGCTTGGGTGGT 900
Dbb 841 CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGCTTGGGTGGT 900
Qy 901 AATCAGTTGGTGATCATTGTGGGAATTGCTGTGCCACAATCCTGCTGCTCCCTGTTCTG 960
Dbb 901 AATCAGTTGGTGATCATTGTGGGAATTGCTGTGCCACAATCCTGCTGCTCCCTGTTCTG 960
Qy 961 ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTCACTGAATTTCTACAGTCTTGGTG 1020
Dbb 961 ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTCACTGAATTTCTACAGTCTTGGTG 1020
Qy 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAACCCCTGCCATTTTGAAGATGT 1080
Dbb 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAACCCCTGCCATTTTGAAGATGT 1080
Qy 1081 GAAGGGGAGAAAACACATTTACTCCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA 1140
Dbb 1081 GAAGGGGAGAAAACACATTTACTCCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA 1140
Qy 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATTGACCCAGTTTGGCCCTCTCTGAGG 1200
Dbb 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATTGACCCAGTTTGGCCCTCTCTGAGG 1200
Qy 1201 TCAGATCGGAACAACTCACTTGAATAAAAGTCAAGTGGGGAATGCCAAAACACAGCAA 1260
Dbb 1201 TCAGATCGGAACAACTCACTTGAATAAAAGTCAAGTGGGGAATGCCAAAACACAGCAA 1260
Qy 1261 GCCTTTTGAGAAGAATGGAGAGTCCCTTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
Dbb 1261 GCCTTTTGAGAAGAATGGAGAGTCCCTTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
Qy 1321 TGTGCTCTGGGCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
Dbb 1321 TGTGCTCTGGGCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
Qy 1381 CTCATTGTTGGTCAATACACTGAAGATGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
Dbb 1381 CTCATTGTTGGTCAATACACTGAAGATGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
Qy 1441 AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGAGCATGGACTTGGCCCTTGAGTGGG 1500
Dbb 1441 AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGAGCATGGACTTGGCCCTTGAGTGGG 1500
Qy 1501 ACACCTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCTCAAAACCCCTGTTGGATCAGACC 1560
Dbb 1501 ACACCTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCTCAAAACCCCTGTTGGATCAGACC 1560
Qy 1561 CTCCTGTGGCAGGGTTCCTTAGTGGATGAGTTACTGGAAGAATCAGAGATAAAACCAA 1620
Dbb 1561 CTCCTGTGGCAGGGTTCCTTAGTGGATGAGTTACTGGAAGAATCAGAGATAAAACCAA 1620
Qy 1621 CCCAAATCAA 1630
Dbb 1621 CCCAAATCAA 1630

RESULT 15

ABX64216

ID ABX64216 standard; cDNA; 1630 BP.

XX ABX64216;

XX 26-FEB-2003 (first entry)

XX cDNA encoding human PRO1387 polypeptide.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;

KW genetic disorder; antibacterial; immunosuppressive; transgenic;

KW gene therapy; gene; ss.

```
XX OS Homo sapiens.
XX OS US2002103125-A1.
XX PN 01-AUG-2002.
XX PD
XX PF 20-NOV-2001; 2001US-00989731.
XX XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 18-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.

PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US0017800.
PR 01-JUN-2001; 2001WO-US0017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX XX
XX (GETH ) GENENTECH LTD.
XX PA
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Pong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX XX
DR WPI; 2003-102117/09.
DR P-PSDB; ABUI3993.
XX XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX XX
PS Claim 2; Fig 303; 649pp; English.
XX XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX SQ
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCGAGTCAGCTGTGGGAGATTTCAGTCGATTGCTCCCTGGGTCTTTCATC 60
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Db 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTCGGCTCTTTCATC 60
Qy 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGCCAGTG 120
Db 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGCCAGTG 120
Qy 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGGCTGAGCTAACAGTC 180
Db 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGGCTGAGCTAACAGTC 180
Qy 181 CATGTGGGTGATTTCAGCTCTGATGGGATGTTTCCAGAGCACAGAAGACAAATGTATA 240
Db 181 CATGTGGGTGATTTCAGCTCTGATGGGATGTTTCCAGAGCACAGAAGACAAATGTATA 240
Qy 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCACGCCAAGGACGAATATGTCTATAC 300
Db 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCACGCCAAGGACGAATATGTCTATAC 300
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Db 301 TATTACTCCAAATCTCAGTGTGCTTATTGGGGCTTCCAGAACCGCGTACACTTGATGGG 360
Qy 361 GACATCTTATGCAATGATGGCTCTCTCCTGTCTCAAGATGTGCAAGGCTGACCAGGGA 420
Db 361 GACATCTTATGCAATGATGGCTCTCTCCTGTCTCAAGATGTGCAAGGCTGACCAGGGA 420
Qy 421 ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA 480
Db 421 ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA 480
Qy 481 CTGCATGTCTTCCAGAGGAGCCCAAGAGCTCATGCTCCATGTGGTGGATTGATTCAG 540
Db 481 CTGCATGTCTTCCAGAGGAGCCCAAGAGCTCATGCTCCATGTGGTGGATTGATTCAG 540
Qy 541 ATGGGATGTGTTTCCAGAGCACAGAACTGAAACACGTTGACCAAGGTAGATGGATATT 600
Db 541 ATGGGATGTGTTTCCAGAGCACAGAACTGAAACACGTTGACCAAGGTAGATGGATATT 600
Qy 601 TCAGGACGGCGGCAAGAGGAGAGATTGTAATTCGTTACTACCAAACTCAGGATGTCT 660
Db 601 TCAGGACGGCGGCAAGAGGAGAGATTGTAATTCGTTACTACCAAACTCAGGATGTCT 660
Qy 661 GTGGAGTACTCCAGAGCTGGGCACTTCCAGAACTGTTGAACCTGGTGGGGACATT 720
Db 661 GTGGAGTACTCCAGAGCTGGGCACTTCCAGAACTGTTGAACCTGGTGGGGACATT 720
Qy 721 TTCCGCAATGACGGTTCCATCATGCTTCAAGAGTGAGGGAGTCAGATGGAGAACTAC 780
Db 721 TTCCGCAATGACGGTTCCATCATGCTTCAAGAGTGAGGGAGTCAGATGGAGAACTAC 780
Qy 781 ACCTGCAGTATCCACCTAGGAACTGTTGTTCAAGAAACCAATTGTGCTGATGTCAGC 840
Db 781 ACCTGCAGTATCCACCTAGGAACTGTTGTTCAAGAAACCAATTGTGCTGATGTCAGC 840
Qy 841 CCGGAAGAGCCTCGAAACACTGTGACCCCGGAGCCCTGAGGCTCTGGTCTTGGGTGGT 900
Db 841 CCGGAAGAGCCTCGAAACACTGTGACCCCGGAGCCCTGAGGCTCTGGTCTTGGGTGGT 900
Qy 901 AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCTGCTGCTCCTGTTCTG 960
Db 901 AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCTGCTGCTCCTGTTCTG 960
Qy 961 ATATTGATCGTGAAGAAGACCTGTGGAAATAGAGTTTCAAGTTCAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAAGACCTGTGGAAATAGAGTTTCAAGTTCAGTCTTGGTG 1020
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Db 1021 AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT 1080
Qy 1081 GAAGGGGAGAAACACATTTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAGAA 1140

Db 1081 GAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAGAA 1140
Qy 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGG 1200
Qy 1201 TCAGATCGGAACAACTCACTTTGAAAAAAGTCAAGTGGGGGAATGCCAAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACAACTCACTTTGAAAAAAGTCAAGTGGGGGAATGCCAAAAACACAGCAA 1260
Qy 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
Db 1261 GCCTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTG 1320
Qy 1321 TGTGTCTGGGCCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTGT 1380
Db 1321 TGTGTCTGGGCCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTGT 1380
Qy 1381 CTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
Db 1381 CTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC 1440
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Db 1441 AGCTCTGGAGGAACAGGCTGCTGAGGGGAGGGAGCATGGACTTGGCCCTTGGAGTGGG 1500
Qy 1501 ACACCTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCCCTCAAAACCCCTTGGATCAGACC 1560
Db 1501 ACACCTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCCCTCAAAACCCCTTGGATCAGACC 1560
Qy 1561 CTCCTGTGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
Db 1561 CTCCTGTGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
Qy 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

Search completed: October 2, 2004, 00:28:37
Job time : 949 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 21:51:10 ; Search time 143 Seconds
(without alignments)
6325.664 Million cell updates/sec

Title: US-09-989-728-421
Perfect score: 1630
Sequence: 1 cggctcgagtcagctgtgg.....taaaaacccaacccaaatcaa 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1621.4	99.5	1751	4	US-09-855-323-11
2	1534.8	94.2	1561	4	US-09-656-952-18
3	1494.8	91.7	1591	4	US-09-656-952-17
4	1483.8	91.0	1592	4	US-09-656-952-1
5	1194.4	73.3	1207	4	US-09-023-655-131
6	609.8	37.4	1024	2	US-08-867-680-1
7	485.6	29.8	1158	4	US-09-663-600A-50
8	485.6	29.8	1158	4	US-09-663-600A-144
9	51.6	3.2	7218	1	US-08-232-463-14
10	40.6	2.5	438	4	US-09-702-705-1549
11	40.6	2.5	438	4	US-09-736-457-1549
12	40.6	2.5	438	4	US-09-614-124B-1549
13	40.6	2.5	438	4	US-09-671-325-1549
14	40.6	2.5	1871	1	US-08-416-478A-1
15	40.6	2.5	1871	2	US-08-474-988B-1
16	40.6	2.5	1871	2	US-08-394-442B-1
17	38.4	2.4	1602	4	US-09-672-494-1
18	38.4	2.4	7872	4	US-08-956-171E-161
19	37	2.3	385	4	US-09-621-976-19314
20	37	2.3	489	4	US-09-621-976-19303
21	35.4	2.2	1275	1	US-08-588-113-1
22	35	2.1	505	4	US-09-621-976-15639
23	35	2.1	1608	4	US-09-134-001C-2407
24	34.6	2.1	526	4	US-09-621-976-16411
25	34.4	2.1	832	4	US-09-621-976-2813
26	34.4	2.1	1073	4	US-09-430-503-25
27	34.4	2.1	1073	4	US-09-430-503-27

28	34.4	2.1	1073	4	US-09-430-503-29	Sequence 29, Appl
29	34.4	2.1	1073	4	US-09-430-503-31	Sequence 31, Appl
30	34.4	2.1	1584	3	US-08-928-383B-1	Sequence 1, Appli
31	34.4	2.1	2434	3	US-09-272-496-1	Sequence 1, Appli
32	34.2	2.1	1489	4	US-09-976-594-730	Sequence 730, App
33	34	2.1	495	4	US-09-134-001C-1793	Sequence 1793, Ap
34	34	2.1	5181	1	US-08-257-073-10	Sequence 10, Appl
35	34	2.1	21784	4	US-09-820-002-3	Sequence 3, Appli
36	33.8	2.1	1164	1	US-08-416-478A-5	Sequence 5, Appli
37	33.8	2.1	1164	2	US-08-474-988B-5	Sequence 5, Appli
38	33.8	2.1	1164	2	US-08-394-442B-5	Sequence 5, Appli
39	33.8	2.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 40	33.6	2.1	1983	1	US-08-073-799C-9	Sequence 9, Appli
41	33.4	2.0	7052	4	US-09-526-193A-22	Sequence 22, Appl
c 42	33	2.0	6426	4	US-09-976-594-136	Sequence 136, App
43	32.8	2.0	1060	4	US-08-997-685A-7	Sequence 7, Appli
44	32.8	2.0	1597	3	US-09-038-832-3	Sequence 3, Appli
45	32.8	2.0	1656	4	US-09-446-301A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-855-323-11
; Sequence 11, Application US/09855323
; Patent No. 6602667
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: Inflammation-Associated Polynucleotides
; FILE REFERENCE: PB-0006-1 CIP
; CURRENT APPLICATION NUMBER: US/09/855,323
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 1751
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 3507924CB1
US-09-855-323-11

Query Match	99.5%	Score 1621.4;	DB 4;	Length 1751;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1622;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	7	GAGTGCAGCTGTGGGAGATTTTCAGTGCATTTCCCTGGGTGCTCTTCACTTGGAT	66	
Db	108	GACTGCAGCTGTGGGAGATTTTCAGTGCATTTCCCTGGGTGCTCTTCACTTGGAT	167	
Qy	67	TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTCTGCCAGTGTACTG	126	
Db	168	TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTCTGCCAGTGTACTG	227	
Qy	127	GATTATTCCTTGGGCTGAATGACCTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG	186	
Db	228	GATTATTCCTTGGGCTGAATGACCTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG	287	
Qy	187	GGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCAGCAAGACAATGTATATTCAAG	246	
Db	288	GGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCAGCAAGACAATGTATATTCAAG	347	
Qy	247	ATAGACTGGACTCTGTCAACAGGAGAGCAGCCCAAGACGAATATGTCTATATTAC	306	
Db	348	ATAGACTGGACTCTGTCAACAGGAGAGCAGCCCAAGACGAATATGTCTATATTAC	407	
Qy	307	TCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCGCGTACACTTGATGGGGACATC	366	
Db	408	TCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCGCGTACACTTGATGGGGACATC	467	

QY 367 TTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAAGGGAACCTAT 426
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Db 468 TTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAAGGGAACCTAT 527
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QY 427 ATCTGTGAAATCCGCTCAAAGGGAGAGCCAGGTGTTCAAGAAGCGGTGTTACTGCAT 486
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Db 528 ATCTGTGAAATCCGCTCAAAGGGAGAGCCAGGTGTTCAAGAAGCGGTGTTACTGCAT 587
|||||
QY 487 GTGCTTCCAGAGAGCCCAAAGAGCTCATGTCATGTGGTGGATGAAATGGATATTTTCAGGA 546
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Db 588 GTGCTTCCAGAGAGCCCAAAGAGCTCATGTCATGTCCTGTTGGTGGATGAAATGGATATTTTCAGGA 647
|||||
QY 547 TGTGTTTTCCAGAGACAGAAAGTGAACACGTCACCAAGGTAGAAATGGATATTTTCAGGA 606
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Db 648 TGTGTTTTCCAGAGACAGAAAGTGAACACGTCACCAAGGTAGAAATGGATATTTTCAGGA 707
|||||
QY 607 CGCGCGCAAGAGGAGATTTGTTTCGTTACTACCAAACTCAGGATGTTCTGGAG 666
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Db 708 CGCGCGCAAGAGGAGATTTGTTTCGTTACTACCAAACTCAGGATGTTCTGGAG 767
|||||
QY 667 TACTCCAGAGCTGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTCCGC 726
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Db 768 TACTCCAGAGCTGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTCCGC 827
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QY 727 AATGACGGTTCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGC 786
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Db 828 AATGACGGTTCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGC 887
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QY 787 AGTATCCACCTAGGAAACCTGGTGTCAAGAAACCATTTGTGCTGATGTCAGCCCGGAA 846
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Db 888 AGTATCCACCTAGGAAACCTGGTGTCAAGAAACCATTTGTGCTGATGTCAGCCCGGAA 947
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QY 847 GAGCTCGAACACTGGTGACCCCGCAGCCCTGAGCCCTCTGGTCTTGGTGGTAATCAG 906
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Db 948 GAGCTCGAACACTGGTGACCCCGCAGCCCTGAGCCCTCTGGTCTTGGTGGTAATCAG 1007
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QY 907 TTGTGATCATTTGGGAAATGTCTGTGCCCAATCTGCTGCTCCCTGTTCTGATATTG 966
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Db 1008 TTGTGATCATTTGGGAAATGTCTGTGCCCAATCTGCTGCTCCCTGTTCTGATATTG 1067
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QY 967 ATCTGGAAGAAGACTGTGGAAATGAAGAGTTCACTGAATTTCTACAGTCTTGGTGAAGAAC 1026
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Db 1068 ATCTGGAAGAAGACTGTGGAAATGAAGAGTTCACTGAATTTCTACAGTCTTGGTGAAGAAC 1127
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QY 1027 ACAGAAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGTGAAGGG 1086
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Db 1128 ACAGAAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGTGAAGGG 1187
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QY 1087 GAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAAGAAGAACCAAGT 1146
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Db 1188 GAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAAGAAGAACCAAGT 1247
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QY 1147 GAAAAATCAGAGGCACCTACATGACCATGCACCAGTTTGGCCTTCTCTGAGGTCAGAT 1206
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Db 1248 GAAAAATCAGAGGCACCTACATGACCATGCACCAGTTTGGCCTTCTCTGAGGTCAGAT 1307
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QY 1207 CGAAACAACTCACTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAAGCCTTT 1266
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Db 1308 CGAAACAACTCACTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAAGCCTTT 1367
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QY 1267 TGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTC 1326
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Db 1368 TGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTC 1427
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QY 1327 CTGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTCTCTCATT 1386
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Db 1428 CTGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTCTCTCATT 1487
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QY 1387 GTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCTGGCAGAGAGACTGGACAGCTCT 1446
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Db 1488 GTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCTGGCAGAGAGACTGGACAGCTCT 1547
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QY 1447 GGAGGAAAGGCCTGCTGAGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTG 1506
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Db 1548 GGAGGAAAGGCCTGCTGAGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTG 1607
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QY 1507 GCCTGGGAACCAAGCTGAGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACCTCCTG 1566
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Db 1608 GCCTGGGAACCAAGCTGAGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACCTCCTG 1667
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QY 1567 TGGCAGGGTTCCTAGTGGATGAGTTACTTGGGAAGAATCAGAGATAAAACCAACCCAAA 1626
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Db 1668 TGGCAGGGTTCCTAGTGGATGAGTTACTTGGGAAGAATCAGAGATAAAACCAACCCAAA 1727
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QY 1627 TCA 1629
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Db 1728 TCA 1730
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RESULT 2
US-09-656-952-18
; Sequence 18, Application US/09656952
; Patent No. 644443
; GENERAL INFORMATION:
; APPLICANT: Gabor Jarai et al.
; TITLE OF INVENTION: No. 644443el Gene
; FILE REFERENCE: 4-31440P1/N1/HO 29
; CURRENT APPLICATION NUMBER: US/09/656,952
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-656-952-18

Query Match 94.2%; Score 1534.8; DB 4; Length 1561;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 44 CTGGGTGCTCTTCATCTTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAAC 103
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Db 2 CCCTGTGCTCTTCATCTTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAAC 61
|||
QY 104 TCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGCCCTGAATGACTTGAATGTTTCCC 163
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Db 62 TCATCCTGCTGCCAGTGTTACTGGATTATACCTTGGCCCTGAATGACTTGAATGTTTCCC 121
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QY 164 CGCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCA 223
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Db 122 CGCTGAGCTAACAGTCCATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCA 181
|||
QY 224 CAGAAAGACAAATGTATATTCAGATAGACTGGACTCTGTACCAGGAGAGCAGCAGCAAGG 283
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Db 182 CAGAAAGACAAATGTATATTCAGATAGACTGGACTCTGTACCAGGAGAGCAGCAGCAAGG 241
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QY 284 ACGAATATGTCTATACTATTACTCCAAATCTCAGTGTGCCTATTGGCGCTTCCAGAAAC 343
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Db 242 ACGAATATGTCTATACTATTACTCCAAATCTCAGTGTGCCTATTGGCGCTTCCAGAAAC 301
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QY 344 GCCTACACTTGTATGGGGACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGC 403
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Db 302 GCCTACACTTGTATGGGGACAACTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGC 361
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QY 404 AAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCAGGTTGT 463
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Db 362 AAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCAGGTTGT 421
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QY 464 TCAAGAAAGCGGTGTTACTGCTGTGCTTCCAGAGGAGCCCAAAGAGCTCATGTTCCATG 523
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Db 422 TCAGGAAGCGGTGTTACTGCTGTGCTTCCAGAGGAGCCCAAAGAGCTCATGTTCCATG 481
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QY 524 TGGGTGGATTGATTGAGATGGGATGTGTTTCCAGAGCAGCAGAAAGTGAACACGTCAGCA 583
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Db 482 TGGGTGGATTGATTGAGATGGGATGTGTTTCCAGAGCAGCAGAAAGTGAACACGTCAGCA 541
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Db 782 TTGTGCTGCATGTACAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGC 841
QY 884 CTCGTGCTTTGGTGGTAATCAGTTGGTGATCATTTGGGGAATTGCTGTGCCACAATCC 943
Db 842 CTCGTGCTTTGGTGGTAATCAGTTGGTGATCATTTGGGGAATTGCTGTGCCACAATCC 901
QY 944 TGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCACTGA 1003
Db 902 TGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCACTGA 961
QY 1004 ATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCCCT 1063
Db 962 ATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCCCT 1021
QY 1064 GCCATTTGAAAGATGTGAAGGGGAG-----AAAC 1093
Db 1022 GCCATTTGAAAGATGTGAAGGGGAGGTGAACACACGCTTCAGCCCTAAACACACTAAAAAC 1081
QY 1094 ACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAAT 1153
Db 1082 ACATTTACTCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAAT 1141
QY 1154 CAGAGGCCACCTACATGACCATGCAACCCAGTTTGGCCTTCTCTGAGTCCAGATCGGAACA 1213
Db 1142 CAGAGGCCACCTACATGACCATGCAACCCAGTTTGGCCTTCTCTGAGTCCAGATCGGAACA 1201
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Db 1202 ACTCACTTGAAAAAAGTCAAGTGGGGGAATGCCAAAAACACAGCAAGCCTTTTGAAAG 1261
QY 1274 AATGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGCC 1333
Db 1262 AATGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGCC 1321
QY 1334 ACTCTACAGTGAATTCAGACTCCCGCTCTCCAGTGTCTCTCCTGTCTCATTTGGT 1393
Db 1322 ACTCTACAGTGAATTCAGACTCCCGCTCTCCAGTGTCTCTCCTGTCTCATTTGGT 1381
QY 1394 CAATACACTGAAGATGGAGAAATTTGAGCCTGGCAGAGACTGGACAGCTCTGGAGGAA 1453
Db 1382 CAATACACTGAAGATGGAGAAATTTGAGCCTGGCAGAGACTGGACAG-TCGGAGGAA 1440
QY 1454 CAGCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGG 1513
Db 1441 CAGCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGG 1500
QY 1514 GAACAGGCTGAGTGAAGTGGCCTCAAAACCCCGTGGATCAGACCCCTCTGTGGGCAG 1573
Db 1501 GAACAGGCTGAGTGAAGTGGCCTCAAAACCCCGTGGATCAGACCCCTCTGTGGGCAG 1560
QY 1574 GGTCTTAGTGGATGAGTTACTGGGAAG 1601
Db 1561 GGTCTTAGTGGATGAGTTACTGGGAAG 1588

RESULT 4

US-09-656-952-1
; Sequence 1, Application US/09656952
; Patent No. 644443
; GENERAL INFORMATION:
; APPLICANT: Gabor Jarai et al.
; TITLE OF INVENTION: No. 644443el Gene
; FILE REFERENCE: 4-31440PI/N1/HO 29
; CURRENT APPLICATION NUMBER: US/09/656.952
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1592
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-656-952-1

Query Match 91.0%; Score 1483.8; DB 4; Length 1592;
Best Local Similarity 97.5%; Pred.No. 0;
Matches 1550; Conservative 0; Mismatches 7; Indels 32; Gaps 3;
Qy 44 CCTGGGTGCTCTTCATCTTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAAC 103
Db 2 CCCTTGTGCTCTTCATCTTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAAC 61
Qy 104 TCATCTGCTGCCAGTGTACTGGATTATTCCTTGGCCCTGAATGACTTGAATGTTTCCC 163
Db 62 TCATCTGCTGCCAGTGTACTGGATTATACCTTGGCCCTGAATGACTTGAATGTTTCCC 121
Qy 164 CGCCTGAGCTAACAGTCCCATGTGGGTGATTGAGTCTGTGATGGATGTTTCCAGAGCA 223
Db 122 CGCCTGAGCTAACAGTCCCATGTGGGTGATTGAGTCTGTGATGGATGTTTCCAGAGCA 181
Qy 224 CAGAAGACAAATGTATATTTCAAGATAGACTGGACTGTGTCCAGAGAGACACGCCAAGG 283
Db 182 CAGAAGACAAATGTATATTTCAAGATAGACTGGACTGTGTCCAGAGAGACACGCCAAGG 241
Qy 284 ACGAATATGTCTATACTATTATTCCTCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC 343
Db 242 ACGAATATGTCTATACTATTATTCCTCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC 301
Qy 344 GCGTACACTTGTATGGGGGACATCTTATGCAATGATGGTCTCTCTCTGCTCCAAGATGTGC 403
Db 302 GCGTACACTTGTATGGGGGACAACTTATGCAATGATGGTCTCTCTCTGCTCCAAGATGTGC 361
Qy 404 AAGAGGCTGACCCAGGGAACCTATATCTGTGAAAATCCGCTTCAAAAGGGAGAGCCAGGTGT 463
Db 362 AAGAGGCTGACCCAGGGAACCTATATCTGTGAAAATCCGCTTCAAAAGGGAGAGCCAGGTGT 421
Qy 464 TCAAGAAAGCGGTGTGCTGATGCTGTGCTTCCAGAGAGCCCAAAGAGTCTCATGTCATG 523
Db 422 TCAGAAAGCGGTGTGCTGATGCTGTGCTTCCAGAGAGCCCAAAGAGTCTCATGTCATG 481
Qy 524 TGGTGGATTGATTAGATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACCGTGAACCA 583
Db 482 TGGTGGATTGATTAGATGGGATGTGTTTCCAGAGCACAGAAAGTGAACACCGTGAACCA 541
Qy 584 AGGTAGAATGGATATTTTCAGGACCGCGCCTCCAGAGTGGGCAATGTTTCTGTTACTACC 643
Db 542 AGGTAGAATGGATATTTTCAGGACCGCGCCTCCAGAGTGGGCAATGTTTCTGTTACTACC 601
Qy 644 ACAAACTCAGGATGTCTGTGGAGTCTCCAGAGTGGGCAATGTTTCTGTTACTACC 703
Db 602 ACAAACTCAGGATGTCTGTGGAGTCTCCAGAGTGGGCAATGTTTCTGTTACTACC 661
Qy 704 ACCTGGTGGGGACATTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAAGGAGT 763
Db 662 ACCTGGTGGGGACATTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAAGGAGT 721
Qy 764 CAGATGGAGGAACTACACCTGCAATGACGGTTCATCATGCTTCAAGGAGTGAAGGAGT 823
Db 722 CAGATGGAGGAACTACACCTGCAATGACGGTTCATCATGCTTCAAGGAGTGAAGGAGT 781
Qy 824 TTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGC 883
Db 782 TTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGC 841
Qy 884 CTCTGGTCTTGGTGGTAATCAGTTGGTGTGATTCATTGTGGGAATTTGTTGCCACAATCC 943
Db 842 CTCTGGTCTTGGTGGTAATCAGTTGGTGTGATTCATTGTGGGAATTTGTTGCCACAATCC 901
Qy 944 TGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAAGTGA 1003
Db 902 TGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAAGTGA 961
Qy 1004 ATTCTACAG-TCCTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCC 1062
Db 962 ATTCTACAGATCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAGAAAAACCC 1021
Qy 1063 TGCCATTTTGAAGAGATGTGAAGGGAG-----AAA 1092

Db 781 ACTCACTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAAGCCTTTTGAGAAG 840
Qy 1274 AATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCCTGGGCC 1333
Db 841 AATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCCTGGGCC 900
Qy 1334 ACTCTACAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTCTCTCATTTGTTGGT 1393
Db 901 ACTCTACAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTCTCTCTCATTTGTTGGT 960
Qy 1394 CAATACACTGAAGATGGAGAAATTTGGAGCTGGCAGAGAGACTGGACAGCTCTGGAGGAA 1453
Db 961 CAATACACTGAAGATGGAGAAATTTGGAGCTGGCAGAGAGACTGGACAGCTCTGGAGGAA 1020
Qy 1454 CAGGCTCTGTAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTGG 1513
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Qy 1514 GAACCAAGCTGAGCTGAGTGGCCTCAAAACCCCGTTGGATCAGACCCCTCTGTGGGCAG 1573
Db 1081 GAACCAAGCTGAGCTGAGTGGCCTCAAAACCCCGTTGGATCAGACCCCTCTGTGGGCAG 1140
Qy 1574 GGTCTTACTGGATGAGTACTGGGAAGAAATCAGAGATAAAAAACCAACCAATCA 1629
Db 1141 GGTCTTACTGGATGAGTACTGGGAAGAAATCAGAGATAAAAAACCAACCAATCA 1196

RESULT 6

US-08-867-680-1
; Sequence 1, Application US/09867680
; Patent No. 5958726
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,680
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-867-680-1

Query Match 37.4%; Score 609.8; DB 2; Length 1024;
Best Local Similarity 99.7%; Pred. No. 1.3e-194;
Matches 611; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GAGTGCAGCTGTGGGAGATTTTCAGTGCATTTCCCTCCCTGGGTGCTCTTCATCTTGGAT 66
Db 2 GACTGCAGCTGTGGGAGATTTTCAGTGCATTTCCCTCCCTGGGTGCTCTTCATCTTGGAT 61
Qy 67 TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTCTGCTGCCAGTGTACTG 126
Db 62 TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTCTGCTGCCAGTGTACTG 121
Qy 127 GATTATTCTTGGCCCTGAATGACITGAATGTTTCCCGCCTGAGCTAAACAGTCCATGTG 186
Db 122 GATTATTCTTGGCCCTGAATGACITGAATGTTTCCCGCCTGAGCTAAACAGTCCATGTG 181
Qy 187 GGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGAAACAAATGTATATTCAAG 246
Db 182 GGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGAAACAAATGTATATTCAAG 241
Qy 247 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCCAAGGACGAATATGTGTATATTATAC 306
Db 242 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCCAAGGACGAATATGTGTATATTATAC 301
Qy 307 TCCAATCTCAGTGTCCCTATTGGGCGCTTCCAGAACCGCGTACACTTGTATGGGGACATC 366
Db 302 TCCAATCTCAGTGTCCCTATTGGGCGCTTCCAGAACCGCGTACACTTGTATGGGGACATC 361
Qy 367 TTATGCAATGATGGCTCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACTAT 426
Db 362 TTATGCAATGATGGCTCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACTAT 421
Qy 427 ATCTGTGAAATCCCGCTCAAAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTACTGCT 486
Db 422 ATCTGTGAAATCCCGCTCAAAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTACTGCT 481
Qy 487 GTGCTTCCAGAGGAGCCCAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGA 546
Db 482 GTGCTTCCAGAGGAGCCCAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGA 541
Qy 547 TGTGTTTTCCAGAGCAGACAGAAAGTGAACACAGCTGACCAAGTAGAATGGATATTTTCAGGA 606
Db 542 TGTGTTTTCCAGAGCAGACAGAAAGTGAACACAGCTGACCAAGTAGAATGGATATTTTCAGGA 601
Qy 607 CGGCGCGCAAAAGG 619
Db 602 CGGCGCGCAAAAGG 614

RESULT 7

US-09-663-600A-50
; Sequence 50, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116

; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 50
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 214..339
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 6.09999990463257
; OTHER INFORMATION: seq AILLQSQAYWA/LP
; NAME/KEY: polyA_signal
; LOCATION: 1133..1138
; NAME/KEY: polyA_site
; LOCATION: 1146..1158
; NAME/KEY: misc_feature
; LOCATION: 840..968
; OTHER INFORMATION: homology
; OTHER INFORMATION: id :H64717
; OTHER INFORMATION: est
; NAME/KEY: misc_feature
; LOCATION: 858..968
; OTHER INFORMATION: homology
; OTHER INFORMATION: id :H65208
; OTHER INFORMATION: est
; NAME/KEY: misc_feature
; LOCATION: 652
; OTHER INFORMATION: n=a, g, c or t
; US-09-663-600A-50

Query Match 29.8%; Score 485.6; DB 4; Length 1158;
Best Local Similarity 98.8%; Pred. No. 9.4e-153;
Matches 496; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 7 GAGTGCAGCTGTGGGAGATTTCAGTGCAATTCGCTCCCTGGGTGCTCTTCATCTTGGAT 66
|||
Db 15 GACTGCAGCTGTGGGAGATTTCAGTGCAATTCGCTCCCTGGGTGCTCTTCATCTTGGAT 74

QY 67 TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGCCAGTGTACTG 126
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Db 75 TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGSTRSAGTG-TAMTG 133

QY 127 GATTATTCCTTGGGCGCTGAATGACTTTGTTCCAGAGCACAGAACGAAATGTATATTCAAG 186
|||
Db 134 GATTATTCCTTGGGCGCTGAATGACTTTGTTCCAGAGCACAGAACGAAATGTATATTCAAG 193

QY 187 GGTGATTGAGTCTGTACCCAGGAGACGCGGACGAAATGTATATTCAAG 246
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Db 194 GGTGATTGAGTCTGTACCCAGGAGACGCGGACGAAATGTATATTCAAG 253

QY 247 ATAGACTGGACTCTGTACCCAGGAGACGCGGACGAAATGTATATTCAAG 306
|||
Db 254 ATAGACTGGACTCTGTACCCAGGAGACGCGGACGAAATGTATATTCAAG 313

QY 307 TCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATC 366
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Db 314 TCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATC 373

QY 367 TTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCCAGGAACCTAT 426
|||
Db 374 TTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCCAGGAACCTAT 433

QY 427 ATCTGTGAAATCCGCCTCAAGGGGAGAGCCAGGTGTTTCAAGAAGCGGTGCTACTGCAT 486
|||
Db 434 ATCTGTGAAATCCGCCTCAAGGGGAGAGCCAGGTGTTTCAAGAAGCGGTGCTACTGCAT 493

QY 487 GTGCTTCCAGAGGAGCCCAAG 508
|||
Db 494 GTGCTTCCAGAGGAGCCCAAG 515

RESULT 8
US-09-663-600A-144
; Sequence 144, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 144
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1133..1138
; NAME/KEY: polyA_site
; LOCATION: 1146..1158
; NAME/KEY: misc_feature
; LOCATION: 652
; OTHER INFORMATION: n=a, g, c or t
; US-09-663-600A-144

Query Match 29.8%; Score 485.6; DB 4; Length 1158;
Best Local Similarity 98.8%; Pred. No. 9.4e-153;
Matches 496; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 7 GAGTGCAGCTGTGGGAGATTTCAGTGCAATTCGCTCCCTGGGTGCTCTTCATCTTGGAT 66
|||
Db 15 GACTGCAGCTGTGGGAGATTTCAGTGCAATTCGCTCCCTGGGTGCTCTTCATCTTGGAT 74

QY 67 TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGCCAGTGTACTG 126
|||
Db 75 TTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGSTRSAGTG-TAMTG 133

QY 127 GATTATTCCTTGGGCGCTGAATGACTTTCCCGGCTGAGCTAACAGTCCATGTG 186
|||
Db 134 GATTATTCCTTGGGCGCTGAATGACTTTCCCGGCTGAGCTAACAGTCCATGTG 193

QY 187 GGTGATTGAGTCTGTATGGGATGTTTTCCAGAGCACAGAACGAAATGTATATTCAAG 246
|||
Db 194 GGTGATTGAGTCTGTATGGGATGTTTTCCAGAGCACAGAACGAAATGTATATTCAAG 253

QY 247 ATAGACTGGACTCTGTACCCAGGAGACGCGGACGAAATGTATATTCAAG 306
|||
Db 254 ATAGACTGGACTCTGTACCCAGGAGACGCGGACGAAATGTATATTCAAG 313

QY 307 TCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATC 366
|||
Db 314 TCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATC 373

QY 367 TTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCCAGGAACCTAT 426

Db 374 TTATGCAATGATGGCTCTCTCTGCTCAAGATGTGCAAGAGGCTGACCAAGGAACTAT 433
QY 427 ATCTGTGAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCAT 486
Db 434 ATCTGTGAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCAT 493
QY 487 GTGCTTCCAGAGGAGCCCAAG 508
Db 494 GTGCTTCCAGAGGAGCCCAAG 515

RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEFAX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgpt-fls
US-08-232-463-14

Query Match 3.2%; Score 51.6; DB 1; Length 7218;
Best Local Similarity 6.8%; Pred. No. 5.6e-06;
Matches 24; Conservative 188; Mismatches 142; Indels 0; Gaps 0;
QY 972 GAAGAAGACTGTGGAATAAGAGTTCAAGTTCAGTGAATCTACAGTCTTGGTGAAGAACAGAA 1031
Db 1368 RRR 1309
QY 1032 GAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTGTAAGATGTGAAGGGGAGAA 1091
Db 1308 RRR 1249

QY 1092 ACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAACCAAGTGAATA 1151
Db 1248 RRR 1189
QY 1152 ATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGGTGAGTCCGAA 1211
Db 1188 RRR 1129
QY 1212 CAATCACTTGAAAAAAGTCAGTGGGGAATGCCAAAAACACAGCAAGCCTTTTGAGA 1271
Db 1128 RRR 1069
QY 1272 AGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTGTGTGT 1325
Db 1068 RRATCGCAAGCTCCCTCGACCTGCAGCAAGCTCGGAATTAATTCTGTGAGCGT 1015

RESULT 10
US-09-702-705-1549
; Sequence 1549, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1549
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1549

Query Match 2.5%; Score 40.6; DB 4; Length 438;
Best Local Similarity 52.0%; Pred. No. 0.0035;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 730 GACGGTTCCATCATGTTCAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAG 789
Db 142 GACTTTACCCCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGGACCTACACCTGCCAT 201
QY 790 ATCCACCTAGGGAACCTGGTGTTCAGAAACCATTGTGCTGCATGTACAGCCCGGAAGAG 849
Db 202 ATCCATCTGCAGGAACAGCAGCTCAATGCCACTGTACATTGGCAATCATCAGTGACT 261
QY 850 CCTCGAACACTGGTGACCCCGGAGCCCTGAGGCTCTGTGCTTTGGGTGTAATC 904
Db 262 CCCAAATCCTTTGGTGCACCTGGATCCCTGGGGAAGCTGCTTTGTGAGGTGACTC 316

RESULT 11
US-09-736-457-1549
; Sequence 1549, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc


```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1724
;
US-08-416-478A-1

Query Match 2.5%; Score 40.6; DB 1; Length 1871;
Best Local Similarity 52.0%; Pred. No. 0.01;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 730 GACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAACTACACCTGCAGT 789
Db 1173 GACTTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGACCTACACCTGCCAT 1232

Qy 790 ATCCACCTAGGGAACTTGTGTTCAAGAAACCAATTTGCTGTCATGTGAGCCCGGAAGAG 849
Db 1233 ATCCATCTGCAGGAACAGCAGCTCAATGCGCACTGTACATTTGGCAATCATCACAGTGACT 1292

Qy 850 CCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGTAATC 904
Db 1293 CCCAAATCCTTTGGGTACCTGGATCCCTGGGGAAGCTGCTTTGTGAGTGACTC 1347

RESULT 15
US-08-474-988B-1
; Sequence 1, Application US/08474988B
; Patent No. 5874250
; GENERAL INFORMATION:
; APPLICANT: Hercend, Thierry
; APPLICANT: Triebel, Frederic
; TITLE OF INVENTION: NEW PROTEINS PRODUCED BY HUMAN
; TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
; TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,988B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,478
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1724
;
US-08-474-988B-1

Query Match 2.5%; Score 40.6; DB 2; Length 1871;
Best Local Similarity 52.0%; Pred. No. 0.01;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 730 GACGGTTCCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAACTACACCTGCAGT 789
Db 1173 GACTTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGACCTACACCTGCCAT 1232

Qy 790 ATCCACCTAGGGAACTTGTGTTCAAGAAACCAATTTGCTGTCATGTGAGCCCGGAAGAG 849
Db 1233 ATCCATCTGCAGGAACAGCAGCTCAATGCGCACTGTACATTTGGCAATCATCACAGTGACT 1292

Qy 850 CCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGTAATC 904
Db 1293 CCCAAATCCTTTGGGTACCTGGATCCCTGGGGAAGCTGCTTTGTGAGTGACTC 1347

Search completed: October 2, 2004, 05:05:29
Job time : 147 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 19:38:55 ; Search time 10107 Seconds
(without alignments)
6990.120 Million cell updates/sec

Title: US-09-989-728-421
Perfect score: 1630
Sequence: 1 cggctcgagtcagctgtgg.....taaaaaaccccaaatcaa 1630

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_htg:

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pl:

9: gb_pr:

10: gb_ro:

11: gb_sts:

12: gb_sy:

13: gb_un:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

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21: em_or:

22: em_ov:

23: em_pat:

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26: em_ro:

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28: em_un:

29: em_vi:

30: em_htg_hum:

31: em_htg_inv:

32: em_htg_other:

33: em_htg_mus:

34: em_htg_pln:

35: em_htg_rod:

36: em_htg_mam:

37: em_htg_vrt:

38: em_sy:

39: em_htgo_hum:

40: em_htgo_mus:

41: em_htgo_other:

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1630	100.0	1630	6	AX403534	Sequence
5	1630	100.0	1630	6	AX454648	Sequence
6	1630	100.0	1630	6	AX464386	Sequence
7	1630	100.0	1630	6	AX491126	Sequence
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9	1621.4	99.5	1751	6	BD248693	Inflammat
10	1621.4	99.5	1751	6	AR373044	Sequence
11	1621	99.4	1635	9	AY138965	Homo sapi
12	1534.8	94.2	1561	6	AR225785	Sequence
13	1534.8	94.2	1561	6	AX347902	Sequence
14	1507.8	92.5	1649	6	BD209975	Human tra
15	1499.8	92.0	1959	6	AX833028	Sequence
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17	1494.8	91.7	1591	6	AR225784	Sequence
18	1494.8	91.7	1591	6	AX347901	Sequence
19	1484.6	91.1	1638	9	HSA515553	Homo sapi
20	1483.8	91.0	1592	6	AR225769	Sequence
21	1483.8	91.0	1592	6	AX347885	Sequence
22	1370.2	84.1	1905	6	AX083427	Sequence
23	1194.4	73.3	1207	6	AR379586	Sequence
24	1011	62.0	1820	6	AX834666	Sequence
25	1011	62.0	1820	9	AK097285	Homo sapi
26	903.2	55.4	916	6	BD139315	Extended
27	846	51.9	5609	9	AK090409	Homo sapi
28	609.8	37.4	1024	6	AR075998	Sequence
29	539.4	33.1	2397	6	AX714902	Sequence
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36	485.6	29.8	1158	6	BD085902	Elongatio
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38	477.4	29.3	1153	6	BD139316	Extended
39	468.4	28.7	1284	10	BC050133	Mus muscu
40	454	27.9	176526	2	AP001192	Homo sapi
41	454	27.9	215441	9	AP002800	Homo sapi
42	454	27.9	215647	2	AC068591	Homo sapi
43	368	22.6	999	6	BD139373	Extended
44	348.2	21.4	469	6	BD058271	Secreted
45	315.6	19.4	345	6	BD247995	5' ESTs f

ALIGNMENTS

RESULT 1
AR252655

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AR252655
Sequence 421 from patent US 6478825.
AR252655
AR252655.1 GI:27300563

1630 bp
DNA
linear
PAT 20-DEC-2002

Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1630)

Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
Implant, method of making same and use of the implant for the
treatment of bone defects

Patent: US 6478825-A 421 12-NOV-2002;

FEATURES		Location/Qualifiers	
source		1..1630	
		/organism="unknown"	
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Query Match 100.0%; Score 1630; DB 6; Length 1630;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCCTCCCTGGGTGCTCTCATC	60
Db	1	CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCCTCCCTGGGTGCTCTCATC	60
QY	61	TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120
Db	61	TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120
QY	121	TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC	180
Db	121	TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC	180
QY	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGCAAGAACAAATGTATA	240
Db	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGCAAGAACAAATGTATA	240
QY	241	TTCAAGATAGACTGGACTCTGTCCAGGAGAGACGCCAAGGACGAATATGTCTATAC	300
Db	241	TTCAAGATAGACTGGACTCTGTCCAGGAGAGACGCCAAGGACGAATATGTCTATAC	300
QY	301	TATTACTCCAATCTCAGTGTGCCATTATGGGCGCTTCAGAAACCGCTACACTTGTATGGG	360
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QY	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA	420
Db	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAGATGTGCAAGAGGCTGACCAAGGA	420
QY	421	ACCTATATCTGTGAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA	480
Db	421	ACCTATATCTGTGAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA	480
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Db	481	CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTGTCATGTGGTGGATTGATTGAG	540
QY	541	ATGGGATGTGTTTCCAGAGCAGAGAGTGAATTCGTTTACTTACCAAACTCAGGATGTCT	600
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Db	601	TCAGGACGGCGCGCAAGAGGAGATTGTTATTTCTGTTACTTACCAAACTCAGGATGTCT	660
QY	661	GTGGAGTACTCCAGAGCTGGGCGCACTTCCAGAAATCGTGTGAACCTGTGGGGACATT	720
Db	661	GTGGAGTACTCCAGAGCTGGGCGCACTTCCAGAAATCGTGTGAACCTGTGGGGACATT	720
QY	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC	780
Db	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC	780
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Db	781	ACCTGCAGTATCCACCTAGGAAACCTGGTGTCAAGAAACCACTTGTGCTCATGTGTCAGC	840
QY	841	CCGGAAGAGCTCGAACACTGTGACCCCGGAGCCCTGAGCCCTCTGCTTGGGTGGT	900
Db	841	CCGGAAGAGCTCGAACACTGTGACCCCGGAGCCCTGAGCCCTCTGCTTGGGTGGT	900
QY	901	AATCAGTTGGTGATCATTTGTGGGAATTTGTCTGTGCCCAATCTGCTGCTCCTGTTCTG	960
Db	901	AATCAGTTGGTGATCATTTGTGGGAATTTGTCTGTGCCCAATCTGCTGCTCCTGTTCTG	960

QY	961	ATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCACTGAATTTCTACAGTCTTGGTG	1020
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QY	1021	AAGAACACGAAAGACCTAATCCAGAGATAAAGAAAAACCTGCCATTTTGAAGATGT	1080
Db	1021	AAGAACACGAAAGACCTAATCCAGAGATAAAGAAAAACCTGCCATTTTGAAGATGT	1080
QY	1081	GAAGGGGAGAAACACATTTCCTCCCAATATTTGTACGGGAGTGCAGGAAAGAA	1140
Db	1081	GAAGGGGAGAAACACATTTCCTCCCAATATTTGTACGGGAGTGCAGGAAAGAA	1140
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QY	1261	GCCTTTTGAGAAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG	1320
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Db	1381	CTCATTTGTTGTTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC	1440
QY	1441	AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGG	1500
Db	1441	AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGG	1500
QY	1501	ACACTGGCCCTGGGAACAGGCTGAGTGGCTCAAAACCCCGTTGGATCAGACC	1560
Db	1501	ACACTGGCCCTGGGAACAGGCTGAGTGGCTCAAAACCCCGTTGGATCAGACC	1560
QY	1561	CTCCTGTGGGCGAGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA	1620
Db	1561	CTCCTGTGGGCGAGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA	1620
QY	1621	CCCAAAATCAA 1630	
Db	1621	CCCAAAATCAA 1630	

RESULT 2	AX358942	Sequence 195 from Patent WO0193983.	DNA	linear	PAT 13-FEB-2002
LOCUS	AX358942	AX358942.1	GI:18675372		
DEFINITION	AX358942				
ACCESSION	AX358942				
VERSION	AX358942.1				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.			
AUTHORS	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
TITLE	Patent: WO 0193983-A 195 13-DEC-2001; Genentech Inc. (US)				
JOURNAL	Location/Qualifiers				
FEATURES	1..1630				
source	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				

ORIGIN		/db_xref="taxon:9606"	
Query Match		100.0%; Score 1630; DB 6; Length 1630;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1630; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	CGGCTCGAGTGCAGTGTGGGGAGATTTCAGTGCAATGCTCCCTGGGTGCTCTTCATC	60
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QY	61	TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGTCAGTG	120
Db	61	TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGTCAGTG	120
QY	121	TTACTGGATTATTCCTTGGGCGCTGAATGACTTGAATGTTTCCCGGCTGAGCTAACAGTC	180
Db	121	TTACTGGATTATTCCTTGGGCGCTGAATGACTTGAATGTTTCCCGGCTGAGCTAACAGTC	180
QY	181	CATGTGGGTGATTCAGCTCTGTATGGGATGTGTTTCCAGAGCAGACGCAAAATGTATA	240
Db	181	CATGTGGGTGATTCAGCTCTGTATGGGATGTGTTTCCAGAGCAGACGCAAAATGTATA	240
QY	241	TTCAAGATAGACTGGACTCTGTACACGAGAGACGCGCAAGGACCAATATGTCTATAC	300
Db	241	TTCAAGATAGACTGGACTCTGTACACGAGAGACGCGCAAGGACCAATATGTCTATAC	300
QY	301	TATTACTCCAAATCTCAGTGTGCTATTTGGGCGTTCAGAACCGCGTACACTTGATGGG	360
Db	301	TATTACTCCAAATCTCAGTGTGCTATTTGGGCGTTCAGAACCGCGTACACTTGATGGG	360
QY	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACACAGGA	420
Db	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACACAGGA	420
QY	421	ACCTATATCTGTGAAATCCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA	480
Db	421	ACCTATATCTGTGAAATCCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA	480
QY	481	CTGCATGTGCTTCCAGAGAGCCCAAAGAGCTCATGTTCCATGTGGTGGATTGATTTCAG	540
Db	481	CTGCATGTGCTTCCAGAGAGCCCAAAGAGCTCATGTTCCATGTGGTGGATTGATTTCAG	540
QY	541	ATGGGATGTGTTTCCAGAGCAGACAGAAAGTGAACACAGTGAACCAAGGTAGATGATATT	600
Db	541	ATGGGATGTGTTTCCAGAGCAGACAGAAAGTGAACACAGTGAACCAAGGTAGATGATATT	600
QY	601	TCAGGACGGCGCGCAAGAGGAGATTGTATTTCTGTTACTACCAAACTCAGGATGTCT	660
Db	601	TCAGGACGGCGCGCAAGAGGAGATTGTATTTCTGTTACTACCAAACTCAGGATGTCT	660
QY	661	GTGGAGTACTCCAGAGTGTGGGCGCACTTCCAGAAATCGTGTGAACCTGTGGGGACATT	720
Db	661	GTGGAGTACTCCAGAGTGTGGGCGCACTTCCAGAAATCGTGTGAACCTGTGGGGACATT	720
QY	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAAGTGAAGAACTAC	780
Db	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAAGTGAAGAACTAC	780
QY	781	ACCTGAGTATCCACCTAGGGAACCTGTTTCAAGAAACCACTTGTGCTCATGTACG	840
Db	781	ACCTGAGTATCCACCTAGGGAACCTGTTTCAAGAAACCACTTGTGCTCATGTACG	840
QY	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGGCGAGCCCTGAGGCCTCTGGTCTTGGGTGGT	900
Db	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGGCGAGCCCTGAGGCCTCTGGTCTTGGGTGGT	900
QY	901	AATCAGTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCCTGCTCCCTGTTCTG	960
Db	901	AATCAGTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCCTGCTCCCTGTTCTG	960
QY	961	ATATTGATCGTGAAGAGACCTGTGGAATAAGAGTTTACAGTCAAGTCTTGGTG	1020
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RESULT 3		AX362435	
LOCUS		1630 bp DNA linear PAT 15-FEB-2002	
DEFINITION		Sequence 195 from Patent WO0208288.	
ACCESSION		AX362435	
VERSION		AX362435.1 GI:18694675	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.	
AUTHORS		Secreted and transmembrane polypeptides and nucleic acids encoding the same	
TITLE		Patent: WO 0208288-A 195 31-JAN-2002;	
JOURNAL		Genentech, Inc. (US)	
FEATURES		Location/Qualifiers	
source		1..1630	
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Query Match									
Best Local Similarity 100.0%; Score 1630; DB 6; Length 1630;									
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTTGCCCTCCCTGGTGTCTTCAATC	60						
QY	61	TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120						
Db	61	TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120						
QY	121	TTACTGGATTATTCCTTGGGCGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAAACAGTC	180						
Db	121	TTACTGGATTATTCCTTGGGCGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAAACAGTC	180						
QY	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGAAACAAATGTATA	240						
Db	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGAGAAACAAATGTATA	240						
QY	241	TTCAAGATAGACTGGACTCTGTCCAGGAGAGACGCCCAAGGACGAATATGTCTATAC	300						
Db	241	TTCAAGATAGACTGGACTCTGTCCAGGAGAGACGCCCAAGGACGAATATGTCTATAC	300						
QY	301	TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGTATGGG	360						
Db	301	TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGTATGGG	360						
QY	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACCAAGGA	420						
Db	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACCAAGGA	420						
QY	421	ACCTATATCTGTGAATCCGCTCAAAAGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA	480						
Db	421	ACCTATATCTGTGAATCCGCTCAAAAGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA	480						
QY	481	CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTGCCATGTGGTGGATTGATTCAG	540						
Db	481	CTGCATGTGCTTCCAGAGGAGCCCAAGAGCTCATGTGCCATGTGGTGGATTGATTCAG	540						
QY	541	ATGGGATGTGTTTTCCAGAGCACAGAACTGAAACACGTCGACCAAGGTAGAATGGATTTT	600						
Db	541	ATGGGATGTGTTTTCCAGAGCACAGAACTGAAACACGTCGACCAAGGTAGAATGGATTTT	600						
QY	601	TCAGGACGGCGGCAAGGAGGAGATTGTATTTGGTTACTACCACAACTCAGGATGTCT	660						
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QY	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGTGGGGGACATT	720						
Db	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGTGGGGGACATT	720						
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QY	781	ACCTGCAGTATCCACCTAGGAACTGGTGTTCAGAAACCACTTGTGCTGCATGTCAGC	840						
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QY	901	AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCTGCTGCTCCCTGTTCTG	960						
Db	901	AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCTGCTGCTCCCTGTTCTG	960						
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Db	961	ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG	1020						
QY	1021	AAGAACACGAAGAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT	1080						

Db	1021	AAGAACACGAAGAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT	1080						
QY	1081	GAAGGGGAGAAAAACACATTTACTCCCAATAATTGTACGGAGGTGATCGAGGAAGAAGAA	1140						
Db	1081	GAAGGGGAGAAAAACACATTTACTCCCAATAATTGTACGGAGGTGATCGAGGAAGAAGAA	1140						
QY	1141	CCAAGTGAATAATCAGAGGCACCTACATGACCATGCACCCAGTTTGGCCCTCTCTGAGG	1200						
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QY	1321	TGTGTCTGGGCCACTCTACCAAGTATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTGT	1380						
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QY	1381	CTCATTTGTTTGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC	1440						
Db	1381	CTCATTTGTTTGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGACTGGAC	1440						
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Db	1441	AGCTCTGGAGGAACAGAGCCTGTCTGAGGGGAGGGAGCATGGACTTGGCCCTCTGGAGTGGG	1500						
QY	1501	ACACTGGCCCTGGGAACACAGGCTGAGCTGAGTGGCTCAACCCCGCTTGGATCAGACC	1560						
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QY	1561	CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA	1620						
Db	1561	CTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAA	1620						
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RESULT 4									
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LOCUS	AX403534	1630 bp	DNA	linear	PAT 14-JUN-2002				
DEFINITION	Sequence 421 from Patent WO0073454.								
ACCESSION	AX403534								
VERSION	AX403534.1	GI:21437009							
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
	1								
AUTHORS	Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,								
	Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,								
	Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,								
TITLE	Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,								
	Williams,P., Wood,W.I. and Zhang,Z.								
	Secreted and transmembrane polypeptides and nucleic acids encoding								
JOURNAL	the same								
	Patent: WO 0073454-A 421 07-DEC-2000;								
	Genentech Inc. (US)								
FEATURES	Location/Qualifiers								
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ORIGIN	/mol_type="unassigned DNA"								
	/db_xref="taxon:9606"								
	Query Match								
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Best Local Similarity 100.0%; Pred. No. 0; Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	CGGTCGAGTGCAGCTGTGGGAGATTTCAGTGCAATTCCTCCCTGGGTGCTCTTCATC	60						
Qy	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120						
Db	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120						
Qy	121	TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC	180						
Db	121	TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC	180						
Qy	181	CATGTGGGTGATTGAGTCTGTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATA	240						
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Qy	241	TTCAAGATAGACTGGACTCTGTCAACAGGAGAGCAGCGCAAGGACGAATATGTGCTATAC	300						
Db	241	TTCAAGATAGACTGGACTCTGTCAACAGGAGAGCAGCGCAAGGACGAATATGTGCTATAC	300						
Qy	301	TATTACTCCAATCTCAGTGTGCTTATTTGGCGCTTCCAGAACCGCGTACACTTGATGGG	360						
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Qy	361	GACATCTTATGCAATGATGGTCTCTCTGCTCAAGATGTGCAAGAGCTGACCAAGGA	420						
Db	361	GACATCTTATGCAATGATGGTCTCTCTGCTCAAGATGTGCAAGAGCTGACCAAGGA	420						
Qy	421	ACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA	480						
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Qy	481	CTGCATGTCTTCCAGAGGAGCCAAAGAGCTCATGGTCCATGTGGTGGATTGATTTCAG	540						
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Qy	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGTGGGGGACATT	720						
Db	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGTGGGGGACATT	720						
Qy	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAACTAC	780						
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Qy	841	CCGGAAGAGCTCGAACACTGGTGACCCCGCAGCCCTGAGCCCTCTGGTCTGGGTGGT	900						
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Qy	901	AATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCTGCTGCCCTGTTCTG	960						
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Db	961	ATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTTCACTGAATTTCAAGTCTTTGGTG	1020						
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Qy	1261	GCCTTTTGAGAAATGGAGAGTCCCTTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTG	1320
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Qy	1561	CTCCTGTGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCAA	1620
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ACCESSION	AX454648		
VERSION	AX454648.1	GI:21713948	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 0208284-A 233 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)		
FEATURES	Location/Qualifiers		
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QY	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCCTGCTGCCAGTG	120						
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QY	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAAGGA	420						
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LOCUS									
DEFINITION									
Sequence 519 from Patent WO0140466.									
ACCESSION									
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VERSION									
AX464386.1 GI:21899209									
KEYWORDS									
SOURCE									
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ORGANISM									
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
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AUTHORS									
Baker, K.P., Beresini, M., Deforge, L., Desnovers, L., Filvaroff, E.,									
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,									
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,									
Wood, W.L. and Zhang, Z.									
TITLE									
Secreted and transmembrane polypeptides and nucleic acids encoding									
same									
JOURNAL									
Patent: WO 0140466-A 519 07-JUN-2001;									
Genentech Inc. (US)									
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Sequence 519 from Patent WO0140466.

AX464386

AX464386.1 GI:21899209

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Baker, K.P., Beresini, M., Deforge, L., Desnovers, L., Filvaroff, E.,

Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,

Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,

Wood, W.L. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding

same

Patent: WO 0140466-A 519 07-JUN-2001;

Genentech Inc. (US)

Location/Qualifiers

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QY	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120			
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QY	121	TACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC	180			
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QY	241	TTCAAGATAGACTGGACTCTGTACCAAGAGACGCCAAGGACGAATATGTCTATAC	300			
Db	241	TTCAAGATAGACTGGACTCTGTACCAAGAGACGCCAAGGACGAATATGTCTATAC	300			
QY	301	TATTACTCCAAATCAGTGTGCTATTTGGGCGTTCAGAACCGCGTACACTTGATGGG	360			
Db	301	TATTACTCCAAATCAGTGTGCTATTTGGGCGTTCAGAACCGCGTACACTTGATGGG	360			
QY	361	GACATCTTATGCAATGATGGTCTCTCCTGTCCAAAGATGTGCAAGAGGCTGACCAAGGA	420			
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QY	421	ACCTATATCTGTGAAATCCGCTCAAGGGAGAGCCAGGTGTTCAAGAAGCGGTGTA	480			
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QY	481	CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGTTCCATGTGGTGGATTGATTCAG	540			
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QY	541	ATGGGATGTGTTTCCAGAGCAGAGAGTGAACACCGTGACCAAGGTAGATGATATT	600			
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QY	1081	GAAGGGGAGAAACACATTTACTCCCCAATAATTTGTACGGGAGGTGATCGAGGAAGAA	1140
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QY	1141	CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG	1200
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LOCUS AX491126 1630 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 233 from Patent WO200690.
ACCESSION AX491126
VERSION AX491126.1 GI:22323900
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 233 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

Query Match 100.0%; Score 1630; DB 9; Length 1630;
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RESULT 9
BD248693
LOCUS

BD248693

1751 bp DNA

linear

PAT 17-JUL-2003

DEFINITION Inflammation-associated genes.
ACCESSION BD248693
VERSION BD248693.1 GI:33058463
KEYWORDS JP 2002530077-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1751)
AUTHORS Walker, M.G., Volkmut, W. and Klingler, T.M.
TITLE Inflammation-associated genes
JOURNAL Patent: JP 2002530077-A 11 17-SEP-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002530077-A/11
PD 17-SEP-2002
PF 04-NOV-1999 JP 2000582557
PR 18-NOV-1998 US 09/195292
PI MICHAEL G WALKER, WAYNE VOLKUT, TOD M KLINGLER PC
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LOCUS AR373044 1751 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 11 from patent US 6602667.
ACCESSION AR373044
VERSION AR373044.1 GI:40074969
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1751)
AUTHORS Walker,M.G., Volkmut,W. and Klingler,T.M.
TITLE Inflammation-associated polynucleotides
JOURNAL Patent: US 6602667-A 11 05-AUG-2003;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Homo sapiens adhesion molecule AMICA (AMICA) mRNA, complete cds.
ACCESSION AY138965
VERSION AY138965.1 GI:27762121
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1635)
AUTHORS Foster, J.S. and Gurney, A.L.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2002) Molecular Biology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
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DEFINITION Sequence 18 from patent US 6444443.
ACCESSION AR225785
VERSION AR225785.1 GI:27263889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1561)
AUTHORS Jarai,G. and Yousefi,S.
TITLE Gene
JOURNAL Patent: US 6444443-A 18 03-SEP-2002;
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RESULT 13
AX347902
LOCUS
DEFINITION Sequence 18 from Patent WO0187938.
ACCESSION AX347902
VERSION AX347902.1 GI:18495708
KEYWORDS
SOURCE Homo sapiens (human)

AX347902 1561 bp DNA linear PAT 01-FEB-2002
Sequence 18 from Patent WO0187938.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Jarai,G. and Yousefi,S.
AUTHORS Novel gene
TITLE Patent: WO 0187938-A 18 22-NOV-2001;
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Qy 224 CAGAAGACAAATGTATATTCAAGATAGACTGGACTCTGTCAACAGGAGAGCAGCCAAAG 283
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RESULT 14
BD209975
LOCUS Human transcriptional regulator molecules.
DEFINITION BD209975 1649 bp DNA linear PAT 17-JUL-2003
ACCESSION BD209975
VERSION BD209975.1 GI:33019745
KEYWORDS JP 2002513554-A/47.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1649)
AUTHORS Hillman,J.L., Bandman,O., Lal,P., Yue,H., Reddy,R., Tang,T.Y.,
Gerstin,E.H., Patterson,C., Baughn,M.R., Azimzai,Y. and Lu,D.A.M.
TITLE Human transcriptional regulator molecules
JOURNAL Patent: JP 2002513554-A 47 14-MAY-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002513554-A/47
PD 14-MAY-2002
PF 04-MAY-1999 JP 2000547113
PR 05-MAY-1998 US 60/084254,07-AUG-1998 US 60/095827 PR
02-OCT-1998 US 60/102745

PI JENNIFER L HILLMAN,OLGA BANDMAN,PREETI LAL,HENRY YUE,ROOPA PI
REDDY,
PI TOM Y TANG,EDWARD H GERSTIN,CHANDRA PATTERSON,MARIAH R BAUGHN,
PI YALDA AZIMZAI,DYUNG AINA M LU
PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/02,A61P43/00,
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FEATURES
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Query Match 92.5%; Score 1507.8; DB 6; Length 1649;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY	283	GACGAATATGTCTATATCTACTATTACTCCAAATCTCAGTGTGCCTATTGGGCGCTTCCAGAAC	342
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QY	403	CAAGAGCTGACCCAGGGAACCTATATCTGTGAATCCGCTCAAAGGGGAGAGCCAGGTG	462
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Db	1299	TGGAGACTCTCTCCTGTGTGTCTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTC	1358
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Db	1599	ATCAGAGATAAAACCAACCAATCA	1625

RESULT 15
AX833028

LOCUS AX833028 1959 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 152 from Patent EP1347046.
ACCESSION AX833028
VERSION AX833028.1 GI:39919163
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

REFERENCE
AUTHORS

Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.

Full-length cDNA sequences									
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Query Match 92.0%; Score 1499.8; DB 6; Length 1959;									
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QY	247	ATAGACTGGACTCTGTCAACAGGAGACACGCCAAGGACGAATATGTGCTATATTATAC	306						
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Search completed: October 2, 2004, 03:17:17
Job time : 10114 secs

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QY	1327	CTGGGCCACTCTACCAAGTGAITTCAGACTCCCGCTCTCCAGCTGTCTCCTGTCTCATT	1386
Db	1655	CTGGGCCACTCTACCAAGTGAITTCAGACTCCCGCTCTCCAGCTGTCTCCTGTCTCATT	1714
QY	1387	GTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCT	1446
Db	1715	GTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCT	1774
QY	1447	GGAGGAACAGGCCTGCTGAGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTG	1506
Db	1775	GGAGGAACAGGCCTGCTGAGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTG	1834
QY	1507	GCCTGGGAACCAAGCTGAGCTGAGTGGCCTCAAAACCCCGCTTGGATCAGACCCCTCTG	1566
Db	1835	GCCTGGGAACCAAGCTGAGCTGAGTGGCCTCAAAACCCCGCTTGGATCAGACCCCTCTG	1894
QY	1567	TGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAAACCAACCCAAA	1626
Db	1895	TGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAAACCAACCCAAA	1954
QY	1627	TCA 1629	
Db	1955	TCA 1957	

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 21:33:56 ; Search time 6328 Seconds
(without alignments)
7692.060 Million cell updates/sec

Title: US-09-989-728-421

Perfect score: 1630

Sequence: 1 cggctcgagtgcagctgtgg.....taaaacacaccccaaatcaa 1630

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vr1:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904.6	55.5	911	29	AY420493 Pan trogl
2	861.6	52.9	898	13	BX402821
3	838.8	51.5	1054	13	BX346274 BX346274
4	836.2	51.3	911	13	BX421455 BX421455

5	828.4	50.8	911	29	AY420492	AY420492 Homo sapi
6	827.4	50.8	915	13	BX414034	BX414034 BX414034
7	800.2	49.1	1015	12	BM921974	BM921974 AGENCOURT
8	791.4	48.6	849	12	BI838890	BI838890 603087272
9	739.8	45.4	1079	13	BX346273	BX346273 BX346273
10	735	45.1	790	12	BI767696	BI767696 603060652
11	730	44.8	758	14	CA306656	CA306656 UI-H-FT1-
12	711.2	43.6	746	14	CD365542	CD365542 UI-H-FT2-
13	691	42.4	710	14	CF541186	CF541186 UI-CF-EC1
14	682.2	41.9	800	12	BI818153	BI818153 603032387
15	663.6	40.7	687	14	CA748568	CA748568 UI-H-FT1-
16	634.2	38.9	804	12	BI521198	BI521198 603081730
17	618.4	37.9	637	13	BQ576128	BQ576128 UI-H-EZ1-
18	601	36.9	818	9	AL048542	AL048542 DXFZp5860
19	600	36.8	740	14	CA444312	CA444312 UI-H-DT1-
20	582.8	35.8	603	12	BM972461	BM972461 UI-CF-EC1
21	569.4	34.9	1050	13	BX383188	BX383188 BX383188
22	559.6	34.3	681	9	AV734642	AV734642 AV734642
23	543	33.3	655	12	BM983629	BM983629 UI-CF-EC1
24	542	33.3	558	9	AW001430	AW001430 wu31d09.x
25	540.8	33.2	590	14	CD690762	CD690762 EST7285 h
26	539.6	33.1	584	10	BE178622	BE178622 PM3-HT060
27	535	32.8	653	13	BQ774379	BQ774379 UI-H-EZ1-
28	528	32.4	556	13	BQ184892	BQ184892 UI-E-EJ1-
29	519.4	31.9	754	14	CD468618	CD468618 LeukoS3 4
30	509.8	31.3	898	13	BX402822	BX402822 BX402822
31	507.4	31.1	532	12	BM931694	BM931694 UI-E-EJ1-
32	497.2	30.5	520	14	CA427055	CA427055 UI-H-DF0-
33	493.8	30.3	498	13	BQ186684	BQ186684 UI-E-EJ1-
34	491.6	30.2	521	10	AW804077	AW804077 PM2-UM008
35	487	29.9	487	10	BF002780	BF002780 7g60h09.x
36	485.4	29.8	764	14	CD467632	CD467632 LeukoS1 5
37	485	29.8	591	14	CD696471	CD696471 EST12994
38	477.2	29.3	699	14	CD528641	CD528641 LeukoN3 3
39	475	29.1	496	13	BQ184472	BQ184472 UI-E-EJ1-
40	471	28.9	482	9	AI291283	AI291283 qm16f09.x
41	451	27.7	721	14	CD366178	CD366178 UI-H-FT1-
42	451	27.7	744	14	CB528873	CB528873 UI-H-FT2-
43	445.8	27.3	449	9	AI185656	AI185656 qe65c08.x
44	437.4	26.8	623	14	CD472358	CD472358 LeukoS6 5
45	426	26.1	463	9	AA043360	AA043360 zk62e11.5

ALIGNMENTS

RESULT 1	AY420493	911 bp	DNA	linear	GSS 12-DEC-2003
AY420493	Pan troglodytes HCM7242 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
LOCUS	AY420493				
DEFINITION	AY420493.1 GI:39776450				
ACCESSION	GSS.				
VERSION	Pan troglodytes (chimpanzee)				
KEYWORDS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.				
SOURCE	1 (bases 1 to 911)				
ORGANISM	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
REFERENCE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
AUTHORS	Science 302 (5652), 1960-1963 (2003)				
JOURNAL	14671302				
PUBMED	2 (bases 1 to 911)				
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
AUTHORS	Direct Submission				
TITLE					

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source Location/Qualifiers
1. .911
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1. .>911
/locus_tag="HCM7242"

ORIGIN

Query Match 55.5%; Score 904.6; DB 29; Length 911;
Best Local Similarity 99.6%; Pred. No. 4.5e-230;
Matches 907; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 85 ATGTTTGCCCACTGAAACTCATCTGCTGCCAGTGTACTGGATTATTCCTTGGGCCTG 144
Db 1 ATGTTTGCCCACTGAAACTCATCTGCTGCCAGTGTACTGGATTATTCCTTGGGCCTG 60

QY 145 AATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTGGTGATTCAGCTCTGATG 204
Db 61 AATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTGGTGATTCAGCTCTGATG 120

QY 205 GGATGTGTTTCCAGAGCACAGAGACAAATGTATATTCAGATAGACTGGACTCTGTCA 264
Db 121 GGATGTGTTTCCAGAGCACAGAGACAAATGTATATTCAGATAGACTGGACTCTGTCA 180

QY 265 CCAGGAGAGCAGCCCAAGGACGATATGTCTATATTTACTTCAATCTCAGTGTGCCT 324
Db 181 CCAGGAGAGCAGCCCAAGGACGATATGTCTATATTTACTTCAATCTCAGTGTGCCT 240

QY 325 ATTGGGCGCTTCAGAAACCGCGTACACTTGATGGGGACATCTTATGCAATGATGGCTCT 384
Db 241 ATTGGGCGCTTCAGAAACCGCGTACACTTGATGGGGACATCTTATGCAATGATGGCTCT 300

QY 385 CTCCTGCTCCAAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCGGCCTC 444
Db 301 CTCCTGCTCCAAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCGGCCTC 360

QY 445 AAAGGGGAGAGCCAGGTGTTCAAGAGGGCGGTGCTGCTGATGCTTCCAGAGAGCCCC 504
Db 361 AAAGGGGAGAGCCAGGTGTTCAAGAGGGCGGTGCTGCTGATGCTTCCAGAGAGCCCC 420

QY 505 AAAGAGCTCATGTTCCATGTGGTGGATTGATTCAGATGGGATGTGTTTCCAGAGCACA 564
Db 421 AAAGAGCTCATGTTCCATGTGGTGGATTGATTCAGATGGGATGTGTTTCCAGAGCACA 480

QY 565 GAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAGAGGAG 624
Db 481 GAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAGAGGAG 540

QY 625 ATTGTATTTCTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGGGC 684
Db 541 ATTGTATTTCTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGGGC 600

QY 685 CACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCGCAATGACGGTTCATCATG 744
Db 601 CACTTCCAGAAATCGTGTGAACCTGGTGGGGACGTTTTCGCAATGACGGTTCATCATG 660

QY 745 CTTCAAGGAGTGAGGAGTCAGATGAGGAAACTACACCTGCAGTATCCACCTAGGAAAC 804
Db 661 CTTCAAGGAGTGAGGAGTCAGATGAGGAAACTACACCTGCAGTATCCACCTAGGAAAC 720

QY 805 CTGGTGTTCAGAAAACCATTTGTGTGTCATGTTCAGTCCGGAAGAGCCTCGAACACTGGTG 864
Db 721 CTGGTGTTCAGAAAACCATTTGTGTGTCATGTTCAGTCCGGAAGAGCCTCGAACACTGGTG 780

QY 865 ACCCGGCGAGCCCTGAGGCCTCTGGTCTTGGTGGTAAATCAGTTGGTGATCATTTGGGGA 924
Db 781 ACCCGGCGAGCCCTGAGGCCTCTGGTCTTGGTGGTAAATCAGTTGGTGATCATTCGTTGGA 840

QY 925 ATTGTCTGTGCCACAATCCTGCTGCTCCCTGCTTCTGATATTGATCGTGAAGAGACCTGT 984
Db 841 ATTGTCTGTGCCACAATCCTGCTGCTCCCTGCTTCTGATATTGATCGTGAAGAGACCTGT 900

QY 985 GGAATAAAGAG 995
Db 901 GGAATAAAGAG 911

RESULT 2
BX402821/c
LOCUS
DEFINITION BX402821 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ006YB01 3-PRIME, mRNA sequence.

ACCESSION BX402821
VERSION BX402821.1 GI:30622916
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 898)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6071.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AJ002ZD01NP1&cluster=6071.r. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS1AJ002ZD01NP1.

FEATURES
source Location/Qualifiers
1. .898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ006YB01"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 52.9%; Score 861.6; DB 13; Length 898;
Best Local Similarity 96.9%; Pred. No. 1.4e-218;
Matches 867; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

QY 719 TTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGAAACT 778
Db 898 TTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGAAACT 839

QY 779 ACACCTGCAGTATCCACCTAGGAACTGGTGTTCAGAAACCATTGTGTCATGTCA 838
Db 838 ACACCTGCAGTATCCACCTAGGAACTGGTGTTCAGAAACCATTGTGTCATGTCA 779

QY 839 GCCCGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCTCTGGTCTGGGTG 898
Db 778 GCCCGAAGAGCCTCGAACACTGGTGACCCCGGAGCCCTGAGGCTCTGGTCTGGGTG 719

QY 899 GTAATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCCTGCTCCTGTTTC 958
Db 718 GTAATCAGTTGGTGATCATTTGTGGGAATTGTCTGTGCCACAATCCTGCTCCTGTTTC 659


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Db      849 GGAMCTGKGTGTTCAAGAAACCATTTGCTGATGTCAGCCGGRAGAG-CTCGAACAC 907
QY      860 TGGTGACCCCGCAGCCCTGAGCCCTCTGGTCTTGGTGGTAAATCAGTTGGTGATCATTG 919
Db      908 TGGTGACCCCGG---CAGCCTGAGSCTCTGGTCTTGGTGGGTAWCAGTTGGTGATMA-TG 963
QY      920 TGGGAATTGCTGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGA 979
Db      964 TGGGATGKYTGTCAMATCTCGCTCCTGTTCTGATWTGATGTGAGAAGACACGAGGAATA 1023
QY      980 CCTGTGGAATAAAGAGTTTCAGTGA 1003
Db     1024 GARTCATKRAYWAAGTTTGGKGA 1047
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RESULT 4
BX421455
LOCUS
DEFINITION
  BX421455 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
  clone CS0DG006YD16 5-PRIME, mRNA sequence.
ACCESSION
  BX421455
VERSION
  BX421455.1 GI:30766084
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 911)
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 6071.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CS0DG006YD16&cluster=6071.r. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CS0DG006YD16
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      /clone="CS0DG006YD16"
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      /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
      with a NotI-oligo(dT) primer. Five prime end enriched,
      double-strand cDNA was digested with Not I and cloned into
      the Not I and EcoRV sites of the pCMVSPORT 6 vector.
      Library was not normalized."
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ORIGIN

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Query Match      51.3%; Score 836.2; DB 13; Length 911;
Best Local Similarity 98.8%; Pred. No. 8.4e-212;
Matches 849; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      5 TCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTCGCTCCCTGGTGTCTTTCATCTTGG 64
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QY      65 ATTTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGCCAGTGTAC 124
Db     113 ATTTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCATCTGCTGCCAGTGTAC 172
QY     125 TGGATTATTCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATG 184
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Db     173 TGGATTATTCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATG 232
QY     185 TGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAAGACAAATGTATATTCA 244
Db     233 TGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAAGACAAATGTATATTCA 292
QY     245 AGATAGACTGGACTCTGTCCAGGAGAGACGCGCAAGGACGAATATGTGTAATACTATT 304
Db     293 AGATAGACTGGACTCTGTCCAGGAGAGACGCGCAAGGACGAATATGTGTAATACTATT 352
QY     305 ACTCCAATCTCAGTGTGCTTATTGGGCGCTTCCAGAAACCGCGTACACTTGTATGGGGACA 364
Db     353 ACTCCAATCTCAGTGTGCTTATTGGGCGCTTCCAGAAACCGCGTACACTTGTATGGGGACA 412
QY     365 TCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTCAAGAGGCTGACCCAGGGAACCT 424
Db     413 TCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTCAAGAGGCTGACCCAGGGAACCT 472
QY     425 ATATCTGTGAATCCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGTAATTC 484
Db     473 ATATCTGTGAATCCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGTAATTC 532
QY     485 ATGTGCTTCCAGAGGAGCCCCAAAGAGCTCATGTGTCATGTGGTGGGATTTGATTCAGATGG 544
Db     533 ATGTGCTTCCAGAGGAGCCCCAAAGAGCTCATGTGTCATGTGGTGGGATTTGATTCAGATGG 592
QY     545 GATGTGTTTTCCAGAGCACAGAAAGTGAACACACCTGACCAAGGTAGAATGGATATTTTCCAG 604
Db     593 GATGTGTTTTCCAGAGCACAGAAAGTGAACACACCTGACCAAGGTAGAATGGATATTTTCCAG 652
QY     605 GACGGCGCGCAAGAGGAGATTGTTTTCGTTTACTACCAAACTCAGGATGCTGTGG 664
Db     653 GACGGCGCGCAAGAGGAGATTGTTTTCGTTTACTACCAAACTCAGGATGCTGTGG 712
QY     665 AGTACTCCCAGAGCTGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCC 724
Db     713 AGTACTCCCAGAGCTGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCC 772
QY     725 GCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGAAACTACACCT 784
Db     773 GCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTYAGATGGAGAAACTACACCT 832
QY     785 GCAGTATCCACCTAGGGAACCT-GGTGTTCAAGAAACCACTTGTGCTGTCATGTGACCCCG 843
Db     833 GCAGTATCCACCTAGGGAACCTGGGTGTTCAAGAAACCACTTGTGCTGTCATGTGACCCCG 892
QY     844 GAAGAGCTTCGAACACTGG 862
Db     893 GAAGAGCTTCGAACACTGG 911
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RESULT 5

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AY420492
LOCUS
DEFINITION
  Homo sapiens HCM7242 gene, VIRTUAL TRANSCRIPT, partial sequence,
  genomic survey sequence.
ACCESSION
  AY420492
VERSION
  AY420492.1 GI:39776449
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 911)
  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
  Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
  Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
  Adams,M.D. and Cargill,M.
  Inferring nonneutral evolution from human-chimp-mouse orthologous
  gene trios
  Science 302 (5652), 1960-1963 (2003)
JOURNAL
  PUBMED
  14671302
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AY420492 911 bp DNA linear GSS 12-DEC-2003

Homo sapiens HCM7242 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY420492 GI:39776449

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 911)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

JOURNAL

PUBMED

14671302

REFERENCE 2 (bases 1 to 911)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
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source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 91.0%; Pred. No. 1e-209;
Matches 829; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 85 ATGTTTGGCCCACTGAAACTCATCTCTGCTGCCAGTGTACTGATTATTCCTTGGGCTG 144
Db |||||||
1 ATGTTTGGCCCACTGAAACTCATCTCTGCTGCCAGTGTACTGATTATTCCTTGGGCTG 60
QY 145 AATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGCGGTGATTCAGTCTGTATG 204
Db |||||||
61 AATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGCGGTGATTCAGTCTGTATG 120
QY 205 GGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAGATAGACTGGACTCTGTCA 264
Db |||||||
121 GGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAGATAGACTGGACTCTGTCA 180
QY 265 CCAGGAGAGCAGCCCAAGGACGAATATGTCTATATTTACTTCCAAATCTCAGTGTGCT 324
Db |||||||
181 CCAGGAGAGCAGCCCAAGGACGAATATGTCTATATTTACTTCCAAATCTCAGTGTGCT 240
QY 325 ATTGGGCGCTTCCAGAACCGCTACACTTGTGGGGACATCTTATGCAATGATGGCTCT 384
Db |||||||
241 ATTGGGCGCTTCCAGAACCGCTACACTTGTGGGGACATCTTATGCAATGATGGCTCT 300
QY 385 CTCCTGTCTCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAATCCGCTC 444
Db |||||||
301 CTCCTGTCTCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAATCCGCTC 360
QY 445 AAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGACTGCTGCTTCCAGAGGAGCCC 504
Db |||||||
361 AAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGACTGCTGCTTCCAGAGGAGCCC 420
QY 505 AAAGAGCTCATGCTCATGTTGGGTGGATTGATTCAGATGGGATGTTTTCAGAGCACA 564
Db |||||||
421 AAAGNN 480
QY 565 GAAGTGAACACAGTGAACCAAGGTAGATGGATATTTTCAGGACGGCGGCAAGAGGAG 624
Db |||||||
481 GAAGNN 540
QY 625 ATTGTATTTGTTTACTACCAAACTCAGGATGCTGTGGAGTACTCCAGAGCTGGGC 684
Db |||||||
541 ATTGTATTTGTTTACTACCAAACTCAGGATGCTGTGGAGTACTCCAGAGCTGGGC 600
QY 685 CACTTCCAGAATCGTGTGAACCTGTTGGGGACATTTTCGCAATGACGGTTCATCATG 744
Db |||||||
601 CACTTCCAGAATCGTGTGAACCTGTTGGGGACATTTTCGCAATGACGGTTCATCATG 660
QY 745 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACTGCAGTATCCACCTAGGGAAC 804
Db |||||||
661 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACTGCAGTATCCACCTAGGGAAC 720
QY 805 CTGGTGTTCAGAAACCATTTGTGCTGATGTGAGCCCGGAAGAGCCTCGAACACTGGTG 864
Db |||||||

Db 721 CTGGTGTTCAGAAAAACCATTTGTGTCATGTTCAGCCCGGAGAGCCTCGAACACTGGTG 780
QY 865 ACCCGGCGAGCCTGAGGCTCTGGTCTTGGTGGTAAATCAGTTGGTATCATTTGGGA 924
Db |||||||
781 ACCCGGCGAGCCTGAGGCTCTGGTCTTGGTGGTAAATCAGTTGGTATCATTTGGGA 840
QY 925 ATTGTCTGTGCCACAATCCTGCTGCTCCCTGTCTGTATTCGTTGAAGAAGACCTGT 984
Db |||||||
841 ATTGTCTGTGCCACAATCCTGCTGCTCCCTGTCTGTATTCGTTGAAGAAGACCTGT 900
QY 985 GGAATAAAGAG 995
Db |||||||
901 GGAATAAAGAG 911
RESULT 6
BX414034/c
LOCUS BX414034 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
DEFINITION clone CS0DG006YD16 3-PRIME, mRNA sequence.
ACCESSION BX414034
VERSION BX414034.1 GI:30767423
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 915)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK046AB11NM1&cluster=6071.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAK046AB11NM1.
FEATURES
Location/Qualifiers
1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG006YD16"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 50.8%; Score 827.4; DB 13; Length 915;
Best Local Similarity 96.7%; Pred. No. 1.9e-209;
Matches 887; Conservative 0; Mismatches 26; Indels 4; Gaps 4;
QY 711 GGGGACATTTTCCGAATGACGGTTCCATCAT-GCTTCAAGGAGTGAGGGAGTCAGATG 769
Db |||||||
914 GGGGACATTTTAAACGCAAAAACGGGTGCTCTCTGGCTCCAAGAAGTGAGGGAGTCAAATG 855
QY 770 GAGGAACTACACCTGCAGTATCCACTAGGGAACCTGGTGTTCAGAAAAACCATTTGTC 829
Db |||||||
854 GAGGAACTTACACCTGCAGGTTCCACTAGGG-ACCTGGTGGTCAAAAAACCAATGTC 796
QY 830 TGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGTGAGCCCGGAGCCTGAGGCCTTGG 889
Db |||||||

Db 795 TGCAAGTCAGCCCGGAAGAGCCTCGAACACTGCTGGCCCCCGGAGCCCTAAGGCCTCTGG 736

Qy 890 TCTTGGGTGTAATCAGTTGGTGATCATTTGGGAATTTCTGTGCCACAATCTGTCTGC 949

Db 735 TCTTGGGTGTAATCAGTTGGTGATCATTTGGGAATTTCTGTGCCACAATCTGTCTGC 676

Qy 950 TCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAAGTGAATTCTA 1009

Db 675 TCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAAGTGAATTCTA 616

Qy 1010 CAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCCTGCCATT 1069

Db 615 CAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATGAAGAAAAACCCCTGCCATT 556

Qy 1070 TTGAAGAAGATGTGAAGGGGAGAAAAACACATTTTACTCCCCCAATAATTGTACGGAGGTGATCG 1129

Db 555 TTGAAGAAGATGTGAAGGGGAGAAAAACACATTTTACTCCCCCAATAATTGTACGGAGGTGATCG 496

Qy 1130 AGGAAGAAGAACCAAGTGAATAATCAGAGGCCACTATACATGACCAATGCACCCAGTTGGC 1189

Db 495 AGGAAGAAGAACCAAGTGAATAATCAGAGGCCACTATACATGACCAATGCACCCAGTTGGC 436

Qy 1190 CTTCTCTGAGGTGAGATCGGAACAACTCATTGAAAAAAGTCAGTGGGGGAATGCCAA 1249

Db 435 CTTCTCTGAGGTGAGATCGGAACAACTCATTGAAAAAAGTCAGTGGGGGAATGCCAA 376

Qy 1250 AAACACAGCAAGCCTTTGGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGAC 1309

Db 375 AAACACAGCAAGCCTTTGGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGAC 316

Qy 1310 TCTCTCTGTGTGTCTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGC 1369

Db 315 TCTCTCTGTGTGTCTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGC 256

Qy 1370 TGTCTCTGTCTCAATTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCCTGGCAG 1429

Db 255 TGTCTCTGTCTCAATTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCCTGGCAG 196

Qy 1430 AGAGACTGGACAGCTCTGGAGGAACAGGCCCTGTGAGGGGAGGGAGCATGGACTTGGCC 1489

Db 195 AGAGACTGGACAGCTCTGGAGGAACAGGCCCTGTGAGGGGAGGGAGCATGGACTTGGCC 136

Qy 1490 TCTGAGTGGGACACTGGCCCTGGGAACAGGCTGAGTGGCTCAAAACCCCGT 1549

Db 135 TCTGAGTGGGACACTGGCCCTGGGAACAGGCTGAGTGGCTCAAAACCCCGC- 77

Qy 1550 TGGATCAGACCCCTCTGTGGGCAGGTTCTTAGTGGATGAGTTACTGGGAAGATCAGAG 1609

Db 76 TGGATCAGACCCCTCTGTGGGCAGGTTCTTAGTGGATGAGTTACT-GGAAGAATCAGAG 18

Qy 1610 ATAAAAACCAACCCAAA 1626

Db 17 ATAAAGGCCAACCCAAA 1

RESULT 7

BM921974

LOCUS

DEFINITION BM921974 1015 bp mRNA linear EST 12-MAR-2002

AGENCOURT 6706977 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753591

5', mRNA sequence.

BM921974

BM921974.1 GI:19372353

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1015)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

AUTHORS

TITLE

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12789 row: j column: 24

High quality sequence stop: 699.

FEATURES

Location/Qualifiers

1..1015

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5753591"

/lab_host="DH10B"

/clone_lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.1%; Score 800.2; DB 12; Length 1015;

Best Local Similarity 99.3%; Pred. No. 3.6e-202;

Matches 835; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 19 GGGGAGATTTCAGTGCATTGCCTCCCTGGTGGTCTTTCATCTTGGATTGAAAGTTGAG 78

Db 29 GGGGAGATTTCAGTGCATTGCCTCCCTGGTGGTCTTTCATCTTGGATTGAAAGTTGAG 88

Qy 79 AGCAGCATGTTTGGCCACTGAACTCATCTGCTGCCAGTGTACTGGATTATTCCTTG 138

Db 89 AGCAGCATGTTTGGCCACTGAACTCATCTGCTGCCAGTGTACTGGATTATTCCTTG 148

Qy 139 GGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAAACAGTCCATGTGGGTGATTCAGCT 198

Db 149 GGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAAACAGTCCATGTGGGTGATTCAGCT 208

Qy 199 CTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAGATAGACTGGACT 258

Db 209 CTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAGATAGACTGGACT 268

Qy 259 CTGTCAACAGGAGAGCAGCCCAAGGAGGCTGACCTTACTTACTCCAATCTCAGT 318

Db 269 CTGTCAACAGGAGAGCAGCCCAAGGAGGCTGACCTTACTTACTCCAATCTCAGT 328

Qy 319 GTGCCTATTGGGCGCTTCCAGAACCGCTACACTTGTGATGGGGACATCTTATGCAATGAT 378

Db 329 GTGCCTATTGGGCGCTTCCAGAACCGCTACACTTGTGATGGGGACATCTTATGCAATGAT 388

Qy 379 GGCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACCAAGGGAACCTATATCTGTGAATC 438

Db 389 GGCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACCAAGGGAACCTATATCTGTGAATC 448

Qy 439 CGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGCTGCTTCCAGAG 498

Db 449 CGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGCTGCTTCCAGAG 508

Qy 499 GAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGATGTTTTTCCAG 558

Db 509 GAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGATGTTTTTCCAG 568

Qy 559 AGCACAGAAAGTGAACACAGCTGACCAAGGTAGAATGGAATTTTTCAGACGGCGGCAAG 618

Db 569 AGCACAGAAAGTGAACACAGCTGACCAAGGTAGAATGGAATTTTTCAGACGGCGGCAAG 628

619 GAGGAGATTGTTATTTCTGTTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGC 678
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 629 GAGGAGATTGTTATTTCTGTTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGC 688
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 679 TGGGGCCACTTCCAGAACTCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCC 738
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 689 TGGGGCCACTTCCAGAACTCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCC 748
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 739 ATCATGCTTCAAGGAGTGAAGGAGTGCAGATGGAGGAACTACACCTGCAGTATCCACCTA 798
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 749 ATCATGCTTCAAGGAGTGAAGGAGTGCAGATGGAGGAACTACACCTGCAGTATCCACCTA 808
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 799 -GGGAACCTGGTGTTCAGAAACCA-TTGTGCTGCATGTGAG-CGCGAAGAGCCTCGA 855
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 809 GGGGAACCTGGTGTTCAGAAACCAATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGA 868
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 856 A 856
 |
 869 A 869

RESULT 8
 BI838890
 LOCUS
 DEFINITION BI838890 849 bp mRNA linear EST 04-OCT-2001
 mRNA sequence.
 ACCESSION BI838890.1 GI:15950440
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 849)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11569 row: 0 column: 18
 High quality sequence start: 5
 High quality sequence stop: 849.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5226473"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_120"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 48.6%; Score 791.4; DB 12; Length 849;
 Best Local Similarity 98.8%; Pred. No. 7.4e-200;
 Matches 839; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
 673 CAGAGCTGGGGCCACTTCCAGAACTCGTGTGAACCTGGTGGGGACATTTTCCGCAATGAC 732

Db	497	CGCTCTCCAGCTGTCT
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Db      339 ACTCTCTCTGTGTGTCCTGGGCCACTCTACACAGTGATTTCAGACTCCCGCTCTCCCA 280
Qy      1368 GCTGTCTCTCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGC 1427
Db      279 GCTGTCTCTCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGC 220
Qy      1428 AGAGAGACTGGACAGCTCTGGAGGAACAGGCTGCTGAGGGAGGGGAGCATGGACTTGG 1487
Db      219 AGAGAGACTGGACAGCTCTGGAGGAACAGGCTGCTGAGGGAGGGGAGCATGGACTTGG 160
Qy      1488 CCTCTGGAGTGGACACTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCTCAAAACCCCCC 1547
Db      159 CCTCTGGAGTGGACACTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCTCAAAACCCCCC 100
Qy      1548 GTTGGATCAGACCTCTGTGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAG 1607
Db      99 GTTGGATCAGACCTCTGTGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAG 40
Qy      1608 AGATAAAACCAACCCAAATCAA 1630
Db      39 AGATAAAACCAACCCAAATCAA 17
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RESULT 12
CD365542/c
LOCUS
DEFINITION
  UI-H-FT2-bjk-a-15-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
  UI-H-FT2-bjk-a-15-0-UI 3', mRNA sequence.
ACCESSION
  CD365542
VERSION
  CD365542.1 GI:31149632
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 746)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-re@mail.nih.gov
  Tissue Procurement: Dr. Gary W. Hunninghake, U of I
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/cgap.html
  Seq primer: M13 FORWARD
  POLYA=Yes.
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FEATURES
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      /tissue_type="Aveolar Macrophage"
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      /lab_host="DH10B (Life Technologies)"
      /clone_lib="NCI-CGAP_FT2"
      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
      modified polylinker; Site_1: EcoR I; Site_2: Not I;
      NCI CGAP_FT2 is a subtraced cDNA library constructed from
      a pool of 81 RNA samples from Alveolar Macrophages
      challenged with different treatments. The library was
      subtraced according to Bonaldo, Lennon and Soares, Genome
      Research, 6:791-806, 1996. The tissue was provided by Dr.
      Gary W. Hunninghake of the University of Iowa.
      TAG_TISSUE=Human Lung Aveolar Macrophage
      TAG_LIB=UI-H-FT2
      TAG_SEQ=GGCCATGCCG"
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ORIGIN

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Query Match      43.6%; Score 711.2; DB 14; Length 746;
Best Local Similarity 99.6%; Pred. No. 1.8e-178;
Matches 713; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      446 AAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGGTACTGTCATGTGCTTCCAGAGAGCCCA 505
Db      743 AAAGGGAGAGCCAGGTGTTCAAGAAAGCGGTGGTACTGTCATGTGCTTCCAGAGAGCCCA 684
Qy      506 AAGAGCTCATGTCCTCATGTGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAG 565
Db      683 AAGAGCTCATGTCCTCATGTGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAG 624
Qy      566 AAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAGAGGAGA 625
Db      623 AAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAGAGGAGA 564
Qy      626 TTGTATTTTCGTACTACCAACAACCTCAGGATGTCTGTGGAGTACTCCAGAGCTGGGGCC 685
Db      563 TTGTATTTTCGTACTACCAACAACCTCAGGATGTCTGTGGAGTACTCCAGAGCTGGGGCC 504
Qy      686 ACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCATCATGC 745
Db      503 ACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCATCATGC 444
Qy      746 TTCAAGGAGTGAAGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGAACC 805
Db      443 TTCAAGGAGTGAAGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGAACC 384
Qy      806 TGGTGTTCAAGAAACCAATTGTGCTGCATGTGAGCCCGGAGAGCCTCGAACACTGGTGA 865
Db      383 TGGTGTTCAAGAAACCAATTGTGCTGCATGTGAGCCCGGAGAGCCTCGAACACTGGTGA 324
Qy      866 CCCCAGCAGCCCTCAGGCGCTCTGGTCTTGGTGGTAATCAGTTGGTATCATTTGTGGAA 925
Db      323 CCCCAGCAGCCCTCAGGCGCTCTGGTCTTGGTGGTAATCAGTTGGTATCATTTGTGGAA 264
Qy      926 TTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACTGTG 985
Db      263 TTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACTGTG 204
Qy      986 GAAATAAGAGTTCAAGTGAATTTCTACAGTCTTGGTGAAGAACACAGAAAGACTAATCCAG 1045
Db      203 GAAATAAGAGTTCAAGTGAATTTCTACAGTCTTGGTGAAGAACACAGAAAGACTAATCCAG 144
Qy      1046 AGATAAAAGAAACCCCTGCCATTTTGAAGATGTGAAGGGGAGAGAAACACATTTACTCCC 1105
Db      143 AGATAAAAGAAACCCCTGCCATTTTGAAGATGTGAAGGGGAGAGAAACACATTTACTCCC 84
Qy      1106 CAATAAATTGTACGGAGGTGATCGAGGAAGAAAGAACCAAGTGAATAATCAGAGGCC 1161
Db      83 CAATAAATTGTACGGAGGTGATCGAGGAAGAAAGAACCAAGTGAATAATCAGAGGCC 28

RESULT 13
CF541186/c
LOCUS
DEFINITION
  UI-CF-EC1-adz-a-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
  UI-CF-EC1-adz-a-24-0-UI 3', mRNA sequence.
ACCESSION
  CF541186
VERSION
  CF541186.1 GI:34593709
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 710)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  JOURNAL
  MEDLINE
  PUBMED
  889548
  COMMENT
    Contact: McCray, PB
```


McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cf.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .710
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="UI-CF-EC1-adz-a-24-0-UI"
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/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 42.4%; Score 691; DB 14; Length 710;
Best Local Similarity 99.6%; Pred. No. 4.4e-173;
Matches 691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 937 ACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAGACCTGTGGAATAAGAGT 996
DB 710 ACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAGACCTGTGGAATAAGAGT 651
QY 997 TCAGTGAATTCTACAGTCTTGGTGAAGACACGAGAGACTAATCCAGAGATAAAAGAA 1056
DB 650 TCAGTGAATTCTACAGTCTTGGTGAAGACACGAGAGACTAATCCAGAGATAAAAGAA 591
QY 1057 AAACCCCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA 1116
DB 590 AAACCCCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA 531
QY 1117 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAATAATCAGAGGCCACCTACATGACCATG 1176
DB 530 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAATAATCAGAGGCCACCTACATGACCATG 471
QY 1177 CACCCAGTTTGGCCTTCTCTGAGGTGATCGGAACAACACTCATTGAAAAAAGTCAGGT 1236
DB 470 CACCCAGTTTGGCCTTCTCTGAGGTGATCGGAACAACACTCATTGAAAAAAGTCAGGT 411
QY 1237 GGGGGAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAG 1296
DB 410 GGGGGAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAG 351

QY 1297 CAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGCCACTCTACCAAGTGATTTTCAGACTC 1356
DB 350 CAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGCCACTCTACCAAGTGATTTTCAGACTC 291
QY 1357 CCGCTCTCCAGCTGCTCCTCCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAATT 1416
DB 290 CCGCTCTCCAGCTGCTCCTCCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAATT 231
QY 1417 TGGAGCCTGGCAGAGACTGGACAGCTCTGGAGGAACAGGCTGCTGAGGGGGGAG 1476
DB 230 TGGAGCCTGGCAGAGACTGGACAGCTCTGGAGGAACAGGCTGCTGAGGGGGGAG 171
QY 1477 CATGGACTTGGCCTCTGGAGTGGGACACTGSCCCTGGGAACCAAGGCTGAGCTGAGTGGCC 1536
DB 170 CATGGACTTGGCCTCTGGAGTGGGACACTGSCCCTGGGAACCAAGGCTGAGCTGAGTGGCC 111
QY 1537 TCAAACCCCGCTTGGATCAGACCCCTCCTGTGGGCAGGGTTCTTAGTGATGAGTTACTG 1596
DB 110 TCAAACCCCGCTTGGATCAGACCCCTCCTGTGGGCAGGGTTCTTAGTGATGAGTTACTG 51
QY 1597 GGAAGAATCAGAGATAAAACCAACCAACCAATCAA 1630
DB 50 GGAAGAATCAGAGATAAAACCAACCAACCAATCAA 17

RESULT 14

BI818153
LOCUS
DEFINITION
BI818153 800 bp mRNA linear EST 04-OCT-2001
mRNA sequence.
ACCESSION
BI818153 GI:15928361
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 800)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11432 row: m column: 21
High quality sequence start: 8
High quality sequence stop: 739.
Location/Qualifiers
1. .800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5173820"
/lab_host="DH10B"
/clone_lib="NIH_MGC 115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

FEATURES

source

1. .800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5173820"
/lab_host="DH10B"
/clone_lib="NIH_MGC 115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN


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QY 1380 TCTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGA 1439
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
267 TCTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGA 208
QY 1440 CAGCTCTGGAGGAAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGG 1499
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
207 CAGCTCTGGAGGAAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGG 148
QY 1500 GACACTGGCCCTGGGAAACAGGCTGAGCTGAGTGGCCTCAAACCCCTTGGATCAGAC 1559
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
147 GACACTGGCCCTGGGAAACAGGCTGAGCTGAGTGGCCTCAAACCCCTTGGATCAGAC 88
QY 1560 CCTCCTGTGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCA 1619
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
87 CCTCCTGTGGCAGGGTTATTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCA 28
QY 1620 ACCCAAATCAA 1630
Db |||||||||||
27 ACCCAAATCAA 17
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Search completed: October 2, 2004, 05:02:57
Job time : 6335 secs

P/ank

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Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 20:59:40 ; Search time 40 seconds
(without alignments)
947.487 Million cell updates/sec

Title: US-09-989-728-422
Perfect score: 2067
Sequence: 1 MFCLPLLLPVLLDYSGL.....RNSLEKSGGMPKTQQAF 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	183	8.9	365	JC7780	coxsackie- and ade
2	147	7.1	584	T08678	hypothetical prote
3	146.5	7.1	246	A32999	myelin P0 protein
4	140.5	6.8	249	A61087	myelin P0 glycopro
5	137	6.6	338	JC4776	limbic-system-asso
6	133	6.4	251	I38053	myelin protein zer
7	132.5	6.4	186	I61783	sodium channel bet
8	132	6.4	248	JH0252	myelin P0 protein
9	131	6.3	219	A29128	myelin P0 protein
10	130	6.3	248	MPRT0	myelin P0 protein
11	127.5	6.2	215	A57843	sodium channel bet
12	126	6.1	1028	A53449	plasmacytoma-assoc
13	125.5	6.1	509	JC5288	SHP substrate-1 pr
14	125.5	6.1	1040	A57638	receptor tyrosine
15	125.5	6.1	1103	T22889	hypothetical prote
16	125.5	6.1	1232	T43027	neural cell adhesi
17	123.5	6.0	285	S36903	Fc gamma (IgG) rec
18	123.5	6.0	1363	I58375	protein-tyrosine k
19	122.5	5.9	247	A54662	myelin P0 protein
20	122.5	5.9	338	JC5519	50K glycoprotein p
21	121.5	5.9	5175	T20992	hypothetical prote
22	121.5	5.9	5198	T43290	hemocentin precurs
23	120.5	5.8	1379	JC4954	vascular endotheli
24	119	5.8	321	I54766	B-lymphocyte activ
25	119	5.8	764	QRHUGS	secretory componen
26	118.5	5.7	317	JL0118	Fc gamma (IgG) rec
27	118.5	5.7	1298	A48999	protein-tyrosine k
28	118	5.7	333	A31923	amalgam protein pr
29	118	5.7	898	A40114	fasciclin II precu

30	116.5	5.6	513	2	JC5289	SHP substrate-1 pr
31	116	5.6	1896	2	T08851	Down syndrome cell
32	115.5	5.6	271	2	A53268	T-cell receptor al
33	114	5.5	847	2	JH0371	B-cell adhesion pr
34	114	5.5	1028	2	I58164	BIG-1 protein - ra
35	111.5	5.4	4391	2	A38096	perlecan precursor
36	111.5	5.4	7962	2	I38346	elastic titin - hu
37	110.5	5.3	330	2	A29915	teratocarcinoma gl
38	109.5	5.3	1323	2	PN0568	connectin 3B - chi
39	109	5.3	1348	2	S51656	vascular endotheli
40	108.5	5.2	299	2	S56749	junctional adhesio
41	108.5	5.2	475	2	I76668	pregnancy-specific
42	108.5	5.2	662	2	T16525	hypothetical prote
43	108.5	5.2	3707	2	S18252	heparan sulfate pr
44	108	5.2	364	2	A30521	myeloid cell surfa
45	107.5	5.2	323	2	S06946	Fc gamma (IgG) rec

ALIGNMENTS

RESULT 1

JC7780
C;Species: and adenovirus receptor - bovine
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C;Accession: JC7780
R;Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto
A;Reference number: JC7780
A;Contents: Liver
A;Accession: JC7780
A;Molecule type: mRNA
A;Residues: 1-365 <THO>
A;Cross-references: GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 8.9%; Score 183; DB 2; Length 365;
Best Local Similarity 23.9%; Pred. No. 1.1e-06;
Matches 95; Conservative 61; Mismatches 146; Indels 96; Gaps 20;

QY	5	LKLILLPVLLDYSGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCFKIDWTLSP 61	
DB	5	LRFLLLCGVADFTRG--LSITTPQMIKAKGETAYLPCKFTLGPEDQGDLIEWLLSP 61	
QY	62	GEHAKDEVVLYYNSNLSPVIGRFQ--RVHL-MGDILNDGSLLLQDVQEQADQGYICE 117	
DB	62	ADNQKVDQVILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTLQLSDIGTYQCK 121	
QY	118	IRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTKVEWIFSGRRA 177	
DB	122	V--KKAPGVGNKKIQLTVL-VKPSGIRCYVDGSEEIGNDFK-----LKCE-----P 164	
QY	178	KE-EIVFRY-YHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIQLQGVRESGGNYTCS 235	
DB	165	KEGSLPLRYEWQKLSQKLPVSW-----LPENTSPV-----ISVKNASAEYSGTYYTCT 213	
QY	236	IHLGNLVFKKTIIVLHVSPEEPRTLVTFAALRPLVLGNQLVIVGIVCATILLPLVILI 295	
DB	214	VR--NRVGSQCLLRDLVVPV-----SNRAGTIAGAVIGTLAL-VLIAL 255	
QY	296	VKKTGKSSVNSTVLVKNTKTNPEIKPKPCFPERCEGEKHIYSPVIVREVIEEERSE 355	
DB	256	IVFCC-----HKRRREEKVEVHHD-----IREDVPPP 284	
QY	356	KSEATYTMHPVWPVSLRSDRNN--SLEKKSGGGMPKTKQ 391	
DB	285	KSRTSTARSY-----IGSNHSSLGSMSPSMEGYSKTKQ 317	

RESULT 2
T08678

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OM protein - protein search, using sw model

Run on: October 1, 2004, 20:51:10 ; Search time 25 Seconds
(without alignments)
820.626 Million cell updates/sec

Title: US-09-989-728-422
Perfect score: 2067
Sequence: 1 MFCPLKILLPVLLDYSIGL.....RNSLEKSKGGMPKTTQAF 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	168	8.1	365	1 CXAR HUMAN	P78310 homo sapien
2	146.5	7.1	246	1 MYP0_HETFR	P20938 heterodontu
3	146	7.1	365	1 CXAR_MOUSE	P97792 mus musculu
4	140.5	6.8	249	1 MYP0_CHICK	P37301 gallus gall
5	138.5	6.7	215	1 CIB2_HUMAN	O60939 homo sapien
6	137	6.6	215	1 EVAL_MOUSE	O70255 mus musculu
7	137	6.6	338	1 LAMP_HUMAN	Q13449 homo sapien
8	135	6.5	338	1 LAMP_RAT	Q62813 rattus norv
9	133	6.4	686	1 IPL2_MOUSE	Q9ers6 mus musculu
10	132	6.4	248	1 MYP0_HUMAN	P25189 homo sapien
11	131	6.3	219	1 MYP0_BOVIN	P10522 bos taurus
12	131	6.3	248	1 MYP0_MOUSE	P27573 mus musculu
13	130	6.3	248	1 MYP0_RAT	P06907 rattus norv
14	128.5	6.2	319	1 A33_HUMAN	Q99795 homo sapien
15	128	6.2	686	1 IPL2_HUMAN	Q9np60 h x-linked
16	127.5	6.2	215	1 CIB2_RAT	P54900 rattus norv
17	127	6.1	316	1 PCGA_PANTR	Q8spv8 pan troglod
18	125.5	6.1	1040	1 EG15_CAEEL	Q10656 caenorhabdi
19	123.5	6.0	285	1 FCG2_RAT	Q63203 rattus norv
20	123.5	6.0	595	1 SILL_HUMAN	Q96pql homo sapien
21	123.5	6.0	1363	1 VGR3_MOUSE	P35917 mus musculu
22	122.5	5.9	338	1 LAMP_CHICK	Q98919 gallus gall
23	120.5	5.8	597	1 SILL_PANTR	Q95lho pan troglod
24	119	5.8	696	1 IPL1_HUMAN	Q9nzn1 homo sapien
25	119	5.8	696	1 IPL1_PANTR	P60029 pan troglod
26	119	5.8	764	1 FIGR_HUMAN	P01833 homo sapien
27	118.5	5.7	317	1 PCGA_HUMAN	P12318 homo sapien
28	118.5	5.7	1298	1 VGR3_HUMAN	P35916 homo sapien
29	118	5.7	333	1 AMAL_DROME	P15364 drosophila
30	118	5.7	898	1 FAS2_SCHAM	P22648 schistocerc
31	117.5	5.7	215	1 EVAL_HUMAN	O60487 homo sapien
32	116.5	5.6	513	1 SHS1_MOUSE	P97797 m protein-t
33	116	5.6	695	1 IPL1_MOUSE	P59823 mus musculu

RESULT 1

ID	CXAR_HUMAN	STANDARD;	PRT;	365 AA.
AC	P78310; O00694;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-adenovirus receptor) (hCAR) (CVB3 binding protein).			
GN	CXADR OR CAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97190109; PubMed=9036860;			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;			
RT	"Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5.";			
RL	Science 275:1320-1323(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97250541; PubMed=9096397;			
RA	Tomko R.P., Xu R., Philipson L.;			
RT	"HCAR and MCAR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20008750; PubMed=10543405;			
RA	Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A., Bowles N.E.;			
RT	"Genomic organization and chromosomal localization of the human Coxsackievirus B-adenovirus receptor gene.";			
RL	Hum. Genet. 105:354-359(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;			
RT	"Sequence and expression of CXADR, the human gene for the coxsackievirus and adenovirus receptor.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Anderson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M., Sollerbrant K., Sonnhammer E., Philipson L.;			
RT	"Putative regulatory domains in the human and mouse CAR genes.";			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cervix;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			

34	116	5.6	2012	1	DSCA_HUMAN	O60469 homo sapien
35	115.5	5.6	298	1	JAM1_BOVIN	Q9xt56 bos taurus
36	115.5	5.6	499	1	SIL8_HUMAN	Q9nyz4 homo sapien
37	115	5.6	696	1	IPL1_RAT	P59824 rattus norv
38	113.5	5.5	4391	1	PGBM_HUMAN	P98160 homo sapien
39	112	5.4	353	1	CEPU_CHICK	Q90773 gallus gall
40	112	5.4	1493	1	NEO1_MOUSE	P97798 mus musculu
41	110.5	5.3	330	1	EMB_MOUSE	P21995 mus musculu
42	110	5.3	215	1	CIB3_MACFA	Q8hxj7 macaca fasc
43	109.5	5.3	879	1	FPRP_HUMAN	Q9p2b2 homo sapien
44	109.5	5.3	1240	1	NFAS_HUMAN	O94856 homo sapien
45	109	5.3	215	1	CIB3_HUMAN	Q9ny72 homo sapien

ALIGNMENTS

CC -!- TISSUE SPECIFICITY: Brain specific.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AF007783; AAC26013.1; -
DR EMBL; AF049498; AAC05274.1; -
DR EMBL; AF049497; AAC05208.1; -
DR EMBL; AF049496; AAC05208.1; JOINED.
DR EMBL; U87555; AAF21472.1; -
DR EMBL; AF107028; AAD47196.1; -
DR EMBL; BC036793; AAH36793.1; -
DR Genew; HGNC:10589; SCN2B.
DR MIM; 601327; -
DR GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR GO; GO:0006814; P:sodium ion transport; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Signal; Immunoglobulin domain; Sodium channel.
FT SIGNAL 1 29
FT CHAIN 30 215
FT DOMAIN 30 159
FT TRANSMEM 160 180
FT DOMAIN 181 215
FT DOMAIN 32 154
FT DISULFID 55 127
FT CARBOHYD 42 42
FT CARBOHYD 66 66
FT CARBOHYD 74 74
FT CONFLICT 2 2
FT CONFLICT 8 8
FT CONFLICT 15 15
FT CONFLICT 48 48
FT CONFLICT 68 68
FT CONFLICT 156 156
FT CONFLICT 178 179
SQ SEQUENCE 215 AA; 24326 MW; 94A30A60A32683F3 CRC64;

Query Match 6.7%; Score 138.5; DB 1; Length 215;
Best Local Similarity 29.2%; Pred. No. 0.00027;
Matches 47; Conservative 25; Mismatches 60; Indels 29; Gaps 6;

Qy 27 PPELTVHVGDSALMGCVFQS--TEDKCFKIDWTLSPGEHAKDEYVLYYSN-LSVPIGR 83
Db 35 PATNLVNLGSDARLPCTFNCSYTVNHKQFSLNWTYQECNCSSEMFQFRMKIINLKLR 94
Qy 84 FQNRVHLMGDLNCNDGSLLLQDVQVQADQGYICEI-----RLKGESQVFKKAVLHVLP 138
Db 95 FQDRVEFSGNPSKYDVSVMLENVQPEDEGIYNCYIMNPPDRHRGHGKIH-----LQVLM 149
Qy 139 EPKE-----LMVHVG-----LIQMGCVFQSTEVK 163
Db 150 EPPERDSTVAVIVGASVGGFLAWILVLMVVKVRRKKEQK 190

RESULT 6
EVAL_MOUSE
ID EVAL_MOUSE STANDARD; PRT; 215 AA.
AC O70255;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Epithelial V-like antigen 1 precursor.
GN EVAL OR EVA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAG-2; TISSUE=Thymus;
RX MEDLINE=98252857; PubMed=9585423;
RA Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
RA Mariani M., Teesalu T., Consalez G.G., Grassi F.;
RT "Epithelial V-like antigen (EVA), a novel member of the immunoglobulin
RT superfamily, expressed in embryonic epithelia with a potential role as
RT homotypic adhesion molecule in thymus histogenesis.";
RL J. Cell Biol. 141:1061-1071(1998).
CC -!- FUNCTION: Mediates homophilic cell-cell adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in liver and gut, skin, and testis
CC but not in thymocytes, lymphocytes, macrophage or dendritic cells
CC or cell lines.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; AF030454; AAC40128.1; -
DR HSSP; P06907; INEU.
DR MGD; MGI:1289160; Eva.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR000920; Myelin_P0.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
KW Signal.
FT SIGNAL 1 26
FT CHAIN 27 215
FT DOMAIN 27 154
FT TRANSMEM 155 175
FT DOMAIN 176 215
FT DOMAIN 27 141
FT DISULFID 47 123
FT CARBOHYD 39 39
FT CARBOHYD 118 118
SQ SEQUENCE 215 AA; 24162 MW; F6E5E36787CE69D5 CRC64;

Query Match 6.6%; Score 137; DB 1; Length 215;
Best Local Similarity 27.1%; Pred. No. 0.00036;
Matches 57; Conservative 33; Mismatches 92; Indels 28; Gaps 9;

Qy 8 ILLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFK-----IDW 57
Db 8 LVLPLLL--SLQLTAL--CPTAEVEITYTSGALEAVNGTDLVRLKCTFSSPAPVGDALTWTW 63
Qy 58 TLSPGEBHAKDEYVLYYSNLSVPI-GRFQNRVHLMGDLNCNDGSLLLQDVQVQADQGYTC 116
Db 64 NFRPRDGGREQVFVYHMDPPFRMSGRFKDRVVDGNGPERYDVSILLWKLQFDNDGTYTC 123
Qy 117 EIR----LKGESQVFKKAVLHVLP-EPEKELMVHVGGLIQMGCVFQSTEV--KHVTKVE 169
Db 124 QVKNPPDVGDLVGTIRLSW-HTVPFSEIYFLAVAIGSACALMIIVIVVWVLFQHFRRKR 182
Qy 170 WI-----FSGRRAKEEIVFRYYHKLMSVE 194

Db 183 WADRADKAEGTKSKEEKLNOGNKVSFVE 212

RESULT 7

LAMP_HUMAN STANDARD; PRT; 338 AA.

AC Q13449;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Limbic system-associated membrane protein precursor (LSAMP).

GN LSAMP OR LAMP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96235133; PubMed=8666243;

RA Pimenta A.F., Fischer I., Levitt P.;

RT "cDNA cloning and structural analysis of the human limbic-system-associated membrane protein (LAMP).";

RL Gene 170:189-195(1996).

CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.

CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF

CC MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH

CC OF THE HYPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: Expressed on limbic neurons and fiber tracts

CC as well as in single layers of the superior colliculus, spinal

CC chord and cerebellum.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON

CC family.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

CC

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CC

DR EMBL; U41901; AAC50569.1; -.

DR PIR; JC4776; JC4776.

DR Genew; HGNC:6705; LSAMP.

DR MIM; 603241; -.

DR GO; GO:0007399; P:neurogenesis; TAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00408; IGC2; 2.

DR PROSITE; PS0835; IG LIKE; 3.

KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;

KW Repeat; Signal; Lipoprotein.

FT SIGNAL 1 28

FT CHAIN 29 315

FT

FT PROPEP 316 338

FT DOMAIN 29 122

FT DOMAIN 132 214

FT DOMAIN 219 304

FT DISULFID 53 111

FT DISULFID 153 197

FT DISULFID 239 290

FT CARBOHYD 40 40

FT CARBOHYD 66 66

FT CARBOHYD 136 136

FT CARBOHYD 148 148

FT CARBOHYD 279 279

FT CARBOHYD 287 287

FT CARBOHYD 300 300

FT CARBOHYD 315 315

FT

FT LIPID 315 315 GPI-anchor amidated asparagine

FT SEQUENCE 338 AA; 37308 MW; 03455F286DF5D92F CRC64;

Query Match 6.6%; Score 137; DB 1; Length 338;

Best Local Similarity 20.1%; Pred. No. 0.00065;

Matches 72; Conservative 54; Mismatches 123; Indels 110; Gaps 14;

QY 4 PLKLILLPVLDYSLGLN--DLNVSPPELTIVHVGDSALMGCVFQSTEDK-----CIF 53

Db 13 PLVLLRLCLLPTGLPVRSDVFRGTNDITVRQDGTALRCVLEDKNSKVAWLNRSGLIF 72

QY 54 --KIDWTLSPGEGHAKDEYVLYYSNLSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQ 111

Db 73 AGHDKWSLDPRVELEKRSLEY-----SLRIQKVDVYDE 106

QY 112 GYICEIRLKGESQVFKKAVLVHVLPE---EPKELMVHVGGLIQMGCVFQSTEV-----K 163

Db 107 GSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEGNSVTLVCMANGRPEPVITWR 166

QY 164 HVTKEVWIFSGR-----RAKEEIVFRYYHKLKMSVEY-----SQS 198

Db 167 HLTPTGREFEGEEYLEILGITRQSGKYCKEAKANEVSSADVQKVTVVNPPTTESKS 226

QY 199 -----WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESGG 230

Db 227 NEATGTRQASLKCEASAVPAPDEFWYRDDTRINSANGLEIKSTEGSSLTVTNVTEHYG 286

QY 231 NYTCSIHLGNLVFKKTIIVLHVSPEPRTLVTTPAALPLVGLGNQNLVIIVGIVCATILL 289

Db 287 NYTC-----VAANKLGVTNAS-----LVLFPRGVRG-INGISLAVPLWLLAASLLCL 334

RESULT 8

LAMP_RAT STANDARD; PRT; 338 AA.

AC Q62813;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Limbic system-associated membrane protein precursor (LSAMP).

GN LSAMP OR LAMP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-49.

RC TISSUE=Hippocampus;

RX MEDLINE=95374785; PubMed=7646886;

RA Pimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,

RA Henzel W., Fischer I., Levitt P.;

RT "The limbic system-associated membrane protein is an Ig superfamily

RT member that mediates selective neuronal growth and axon targeting.";

RL Neuron 15:287-297(1995).

CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.

CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF

CC MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH

CC OF THE HYPOCAMPAL MOSSY FIBER PROJECTION.

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: Expressed mostly by neurons comprising limbic-

CC associated cortical and subcortical regions that function in

CC cognition, emotion, memory, and learning.

CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS

CC DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE

CC THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN

CC HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALE AND MEDIAL THALAMIC

CC REGION.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON

CC family.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

CC

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DR EMBL; U31554; AAA86120.1; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 28
FT CHAIN 29 315
FT
FT LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROTEIN.
FT PROPEP 316 338
FT DOMAIN 29 122
FT DOMAIN 132 214
FT DOMAIN 219 304
FT DISULFID 53 111
FT DISULFID 153 197
FT DISULFID 239 290
FT CARBOHYD 40 40
FT CARBOHYD 66 66
FT CARBOHYD 136 136
FT CARBOHYD 148 148
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 300 300
FT CARBOHYD 315 315
FT LIPID 315 315
SQ SEQUENCE 338 AA; 37324 MW; 0B76AFDD68A39BB6 CRC64;

Query Match 6.5%; Score 135; DB 1; Length 338;
Best Local Similarity 19.8%; Pred. No. 0.00095;
Matches 71; Conservative 55; Mismatches 123; Indels 110; Gaps 14;

QY 4 PLKLLPVLDDYSLGN--DLNVSPPELTIVHVGDSALMGCVFQSTEDK-----CIF 53
Db 13 PLVLLRLCLLPTGLPVRSDVFNRTGDTNITVRQGDITAILRCVVEDKNSKVAWLNRSIIF 72
QY 54 --KIDWTLSPGEHAKDEYVLYYNSLNSVPICRFQNRVHLMGDLICNDGSLLLQDVQEAQ 111
Db 73 AGHDKWSLDRPVELEKRHALEY-----SLRIQKVDVYDE 106
QY 112 GTYICEIRLKGESQVFKKAVLVHLPE---EPKELMVHVGGLIQMGCVFQSTEV-----K 163
Db 107 GSYTCVQVQHEPKTSQVYLIVQVPPKISNTSSDVTNVEGNSVTLVCMANGRPEPVITWR 166
QY 164 HVTKEVWIFSGR-----RAKEEIVFRYHKLKRMVSEY-----SQS 198
Db 167 HLTPLGREFEFGEYEELEILGITREQSGKYECKAANEVSSADVQVKVTVNVPPTITESKS 226
QY 199 -----WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESGG 230
Db 227 NEATTGRQASLKCEASAVPAPDFEYWRDTRINSANGLEIKSTEGQSSTLVNTVTEHYG 286
QY 231 NYTCSIHLGNLVFKKTIIVLHVSPPEPRTLVTAAALRPLVLGGNQLVIVGIVCATILL 289
Db 287 NYTC-----VAANKLGVTNAS----LVLFPGSVRG-INGSISLAVPLWLLAASLFCL 334

RESULT 9
IPL2_MOUSE
ID IPL2_MOUSE STANDARD; PRT; 686 AA.
AC Q9ERS6; Q9ER66;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
GN (IL1RAPL-2 related protein) (TIGIR-1).
OC IL1RAPL2.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Liver;
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L.; Smith D.E.; Garka K.E.; Renshaw B.R.; Bertles J.S.;
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21472256; PubMed=11587848;
RA Ferrante M.I.; Ghiani M.; Bulfone A.; Franco B.;
RT "IL1RAPL2 maps to Xq22 and is specifically expressed in the central
RT nervous system.";
RL Gene 275:217-221(2001).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9ERS6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ERS6-2; Sequence=VSP_008056, VSP_008057;
CC Note=may be due to an intron retention;
CC -!- TISSUE SPECIFICITY: Detected in fetal brain after day 12.5, in
CC particular in parts of the diencephalon and in the basal plate of
CC the spinal cord. In postnatal brain detected in cerebral cortex,
CC olfactory bulb, in the CA1 region of the hippocampus and in
CC Purkinje cells of the Xth cerebellar lobule.
CC -!- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 TIR domain.

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DR EMBL; AF284437; AAG21371.1; -;
DR EMBL; AJ277831; CAC10559.1; -;
DR MGD; MGI:1913106; Il1rapl2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR004077; IL1_receptor1p.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01539; INTRLEUKNIR2.
DR PRINTS; PR01537; INTRLEUKNIRIF.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50104; TIR; 1.
KW Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 686
FT X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
FT PROTEIN-LIKE 2.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT DOMAIN 17 354
FT TRANSMEM 355 375

RT "Complete amino acid sequence of P0 protein in bovine peripheral
RT nerve myelin.";
RL J. Biol. Chem. 262:4208-4214(1987).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-GLYCANS IS SULFATED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
DR A29128; A29128.
DR HSP; P06907; INEU.
DR GlycoSuiteDB; P10522; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00568; MYELIN_P0; 1.
KW Myelin; Structural protein; Glycoprotein; Transmembrane;
KW Phosphorylation; Immunoglobulin domain.
FT DOMAIN 1 124 EXTRACELLULAR.
FT TRANSMEM 125 150
FT DOMAIN 151 219
FT DOMAIN 1 114
FT DISULFID 21 98
FT CARBOHYD 93
FT MOD_RES 181 181
FT MOD_RES 204 204
FT MOD_RES 214 214
SQ SEQUENCE 219 AA; 24710 MW; B4A882C1B7225FAF CRC64;

Query Match 6.3%; Score 131; DB 1; Length 219;
Best local similarity 26.2%; Pred. No. 0.0011;
Matches 42; Conservative 27; Mismatches 73; Indels 18; Gaps 5;

QY 141 KLMVHVHGLIQMGCVFQSTE-VKHVTKVEWIFSGRAKEEIVFRVYHKLMSVEYSQSW 199
Db 7 KEVHGAAGVSGVTLVCSFWSSEWSDLSFTWRYQPEGGRDAISIFHYAK---GQPIDEV 63

QY 200 GHFQNRVNLVGDIFRNDGSMIQGVRESGDNNTCSIHGLNLFVFKKT--IVLHVSPEEPR 257
Db 64 GTFEXRIQWGDPRHKGDSIVIHNLVDYDNGTFTCDVKNPPDIVGKTSQVTLVYFVKVPT 123

QY 258 TLVTPAALRPLVGLGNLQVIVGIVCATILLPVLILIVK 297
Db 124 RY-----GVVLGA-----VIGGVLGVLLALLFLYLIR 151

RESULT 12
MYP0_MOUSE
ID MYP0_MOUSE STANDARD; PRT; 248 AA.
AC P27573;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
DE protein) (MPP).
GN MPZ OR P0.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=1709914;
RX MEDLINE=91244320; PubMed=1709914;
RA You K.H., Hsieh C.L., Hayes C., Stahl N., Francke U., Popko B.;
RT "DNA sequence, genomic organization, and chromosomal localization of
RT the mouse peripheral myelin protein zero gene: identification of
RT polymorphic alleles.";

RL Genomics 9:751-757(1991).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-LINKED GLYCANS IS SULFATED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M62860; AAA39867.1; -.
CC EMBL; M62857; AAA39867.1; JOINED.
CC EMBL; M62858; AAA39867.1; JOINED.
CC EMBL; M62859; AAA39867.1; JOINED.
CC HSP; P06907; INEU.
CC MGD; MGI:103177; Mpz.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig v.
CC InterPro; IPR000920; Myelin_P0.
CC PRINTS; PR00213; MYELINP0.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC PROSITE; PS00568; MYELIN_P0; 1.
KW Myelin; Structural protein; Glycoprotein; Transmembrane;
KW Phosphorylation; Immunoglobulin domain; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 248 MYELIN P0 PROTEIN.
FT DOMAIN 30 153 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 154 179 BY SIMILARITY.
FT DOMAIN 180 248 CYTOPLASMIC (BY SIMILARITY).
FT DOMAIN 30 143 IG-LIKE V-TYPE.
FT DISULFID 50 127 POTENTIAL.
FT CARBOHYD 122 122 N-LINKED (GLCNAC..) (COMPLEX).
SQ SEQUENCE 248 AA; 27621 MW; 936D66684300CAC9 CRC64;

Query Match 6.3%; Score 131; DB 1; Length 248;
Best local similarity 25.4%; Pred. No. 0.0014;
Matches 45; Conservative 32; Mismatches 80; Indels 20; Gaps 6;

QY 124 SQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVEWIFSGRAKEEIV 182
Db 21 SLVLSPALAIVVYTD--REIYGAVGSGVTLVHCSFWSSEWSDLSFTWRYQPEGGRDAIS 78

QY 183 FRYVHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSMIQGVRESGDNNTCSIHGLNIV 242
Db 79 IFHYAK---GQPIDEVGAFKERIQWGDPRWKGDSIVIHNLVDYDNGTFTCDVKNPPDI 135

QY 243 FKKT--IVLHVSPEEPRTLVTPAALRPLVGLGNLQVIVGIVCATILLPVLILIVK 297
Db 136 VGKTSQVTLVYFVKVPTRY-----GVVLGA-----VIGGVLGVLLALLFLYLIR 180

RESULT 13
MYP0_RAT
ID MYP0_RAT STANDARD; PRT; 248 AA.
AC P06907;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
DE protein) (MPP).
GN MPZ OR P0.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR004077; IL1_receptorIIP.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01539; INTRLEUKN1R2.
DR PRINTS; PR01537; INTRLEUKN1R1F.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS50104; TIR; 1.
KW Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 686 X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
FT PROTEIN-LIKE 2.
FT DOMAIN 17 354 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 355 375 POTENTIAL.
FT DOMAIN 376 686 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 132 IG-LIKE C2-TYPE 1.
FT DOMAIN 141 232 IG-LIKE C2-TYPE 2.
FT DOMAIN 239 347 IG-LIKE C2-TYPE 3.
FT DOMAIN 400 559 TIR.
FT DISULFID 53 116 POTENTIAL.
FT DISULFID 162 214 POTENTIAL.
FT DISULFID 265 331 POTENTIAL.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 686 AA; 78669 MW; E400F7ECD186957C CRC64;

Query Match 6.2%; Score 128; DB 1; Length 686;
Best Local Similarity 20.3%; Pred. No. 0.0091;
Matches 80; Conservative 60; Mismatches 135; Indels 120; Gaps 19;

QY 25 VSPPELTVHVGDSSALMGCVFQSTEDKCFK-----IDWTLIS-----DGSLLLQDVQEQADQGY 114
Db 1 MKPPFLL-----ALVVCVVSTNLKMKVSKNSVDGCIDWSVDLKTYYMALAGEPVRVKCA 54

QY 71 LYY-----YS---NLSVPIGRFQNRVHLMGDILCN-----DGSLLLQDVQEQADQGY 114
Db 55 LFYSYIRTYNSTAQSTGLRLMWYKNGDLEPIIFSEVRMSKEEDSIWFHSAEAQDSGFY 114

QY 115 ICEIRLKGESQVFKKAVLVHLPPEEPKELMHVHGGLIQMGCVFQS----TEVKHVTKVEW 170
Db 115 TCVLR--NSTYCMKVSMSTVAENE-----SGLCYNSRIRYLEKSEVTKRKE 159

QY 171 I-----PSGRRAKEEIVFRYYHKLKRMVSEYSQSWGHFQNRVNLVGDIFRNDGSLMLQ 223
Db 160 ISCPDMDDFKKSDDQEPDVVWYKECKPKM-----WRSI-----IIQGNALLIQE 203

QY 224 VRESGGNYTCSIHLGNLVFKKTIIVLHVSPEEPRTLVTTPAALRPLVLGGNQLVII----- 278
Db 204 VQEEGGNYTCELKYEGLVRRTTTELKVT-----ALLTDKPKPLFPMPENQPSVIDVQLG 258

QY 279 --VGIVCATILL-----PVL-----ILLVKKTCGNKSSVNSTVL 311
Db 259 KPLNIPCKAFFGSGESGPMIYWMKGEKFIIBELAGHIREGEIRLLKEHLGEK-EVELALI 317

QY 312 VKNTKKTNPEIKKPCPFCECEGEKHIYSPILVRE 346
Db 318 FDSV--VEADLANYTCHVENRNGRKH--ASVLLRK 348

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 20:58:27 ; Search time 119 Seconds
(without alignments)
1044.657 Million cell updates/sec

Title: US-09-989-728-422
Perfect score: 2067
Sequence: 1 MFCPLKILLPVLLDYSGL.....RNNSLEKSGGMPKTQAF 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2067	100.0	394	4	Q86YT9 homo sapien
2	1985	96.0	384	4	Q8N9I7 homo sapien
3	1783	86.3	394	4	Q7Z499 homo sapien
4	1364	66.0	283	4	Q8NF70 homo sapien
5	982	47.5	379	11	Q80UL9 mus musculus
6	198	9.6	335	13	Q9YGV5 gallus gall
7	192	9.3	335	13	Q9PWR4 gallus gall
8	191	9.2	335	13	Q9YGH1 gallus gall
9	183	8.9	365	6	Q8WMV3 bos taurus
10	168	8.1	344	4	Q9UKV4 homo sapien
11	167	8.1	2828	4	Q9NR99 homo sapien
12	164	7.9	319	6	Q9TU80 canis famil
13	158	7.6	373	4	Q9H6B4 homo sapien
14	154.5	7.5	373	11	Q920S5 mus musculus
15	152.5	7.4	372	11	Q8K1G0 rattus norv
16	152	7.4	319	6	Q9TU79 sus scrofa

17	151.5	7.3	437	13	Q90WI4	Q90wi4 gallus gall
18	151	7.3	372	13	Q90Y50	Q90y50 brachydanio
19	150.5	7.3	373	11	Q8R373	Q8r373 mus musculus
20	147.5	7.1	243	4	Q9UEL4	Q9uel4 homo sapien
21	147.5	7.1	269	4	Q95297	Q95297 homo sapien
22	147	7.1	330	11	P97269	P97269 cavia porce
23	147	7.1	344	11	Q9R067	Q9r067 rattus norv
24	147	7.1	358	11	Q9R066	Q9r066 rattus norv
25	147	7.1	584	4	Q9Y3Y8	Q9y3y8 homo sapien
26	146	7.1	352	11	Q91W66	Q91w66 mus musculus
27	146	7.1	365	11	Q9DBJ8	Q9dbj8 mus musculus
28	144.5	7.0	183	4	Q9UEL6	Q9uel6 homo sapien
29	144.5	7.0	209	4	Q9NYK4	Q9nyk4 homo sapien
30	142.5	6.9	202	4	Q8IX11	Q8ix11 homo sapien
31	142	6.9	337	11	P97268	P97268 cavia porce
32	140	6.8	215	11	Q91WI4	Q91wi4 mus musculus
33	139.5	6.7	329	13	Q9IAY6	Q9iay6 spherooides
34	138.5	6.7	318	13	Q91664	Q91664 xenopus lae
35	137.5	6.7	907	5	Q9NEG0	Q9neg0 drosophila
36	137.5	6.7	3215	5	Q8IRV7	Q8irv7 drosophila
37	137.5	6.7	4117	5	Q8IRV9	Q8irv9 drosophila
38	137.5	6.7	4179	5	Q9W4Y4	Q9w4y4 drosophila
39	137.5	6.7	4223	5	Q8MPN3	Q8mpn3 drosophila
40	137.5	6.7	4228	5	Q8IRV8	Q8irv8 drosophila
41	136	6.6	338	4	Q8IV49	Q8iv49 homo sapien
42	136	6.6	339	13	Q9IAZ1	Q9iaz1 spherooides
43	135.5	6.6	199	13	Q8JG36	Q8jg36 brachydanio
44	134.5	6.5	403	6	Q9N2H5	Q9n2h5 equus cabal
45	134	6.5	252	4	Q8WWT6	Q8wwt6 homo sapien

ALIGNMENTS

RESULT 1
Q86YT9
ID Q86YT9 PRELIMINARY; PRT; 394 AA.
AC Q86YT9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Adhesion molecule AMICA.
GN AMICA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Foster J.S., Gurney A.L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY138965; AAN52117.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG. 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 394 AA; 44339 MW; 64B542F9384C7642 CRC64;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFCPLKILLPVLLDYSGLNDLVNPSPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKILLPVLLDYSGLNDLVNPSPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Qy 61 PGEHAKDEYVLYYYNSLVSPIGRFQNRVHLMGDI LCN DGSLL LLDVQVQADQGT YICEIRL 120
Db 61 PGEHAKDEYVLYYYNSLVSPIGRFQNRVHLMGDI LCN DGSLL LLDVQVQADQGT YICEIRL 120
Qy 121 KGESQVFKKAVLVHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHKVTKEWIFSGRRAKEE 180
Db 121 KGESQVFKKAVLVHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHKVTKEWIFSGRRAKEE 180

ID Q8NF70 PRELIMINARY; PRT; 283 AA.
AC Q8NF70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FLJ00300 protein (Fragment).
GN FLJ00300.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
spleen."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090409; BAC03390.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 1
SQ SEQUENCE 283 AA; 32079 MW; CCACBSB0839EB30E CRC64;

Query Match 66.0%; Score 1364; DB 4; Length 283;
Best Local Similarity 99.2%; Pred. No. 7.3e-117;
Matches 257; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 25 MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 84
QY 61 PGEHAKDEVLYYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQVQADQGTIYCEIRL 120
Db 85 PGEHAKDEVLYYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQVQADQGTIYCEIRL 144
QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
Db 145 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 204
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSIH LGN 240
Db 205 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSIH LGN 264
QY 241 LVFKKKTIVLHVSPEEPRTL 259
Db 265 LVFKKKTIVLHVSPEEPSI 283

RESULT 5
Q80UL9
ID Q80UL9 PRELIMINARY; PRT; 379 AA.
AC Q80UL9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to adhesion molecule AMICA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B5/EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050133; AAH50133.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 379 AA; 42561 MW; 2CCOF2987CB12B7F CRC64;
Query Match 47.5%; Score 982; DB 11; Length 379;
Best Local Similarity 56.1%; Pred. No. 1.3e-81;
Matches 222; Conservative 35; Mismatches 105; Indels 34; Gaps 9;
QY 1 MFCPLKLILLPVLL---DYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDW 57
Db 1 MLCCLKLIVIPVILAPVGPQGLPGLTVSSPQLRVHVGESVLMGCVVQRTTEKHVDRVDW 60
QY 58 TLSPGCEHAKDEVLYYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQVQADQGTIYCE 117
Db 61 LFSKDKDDASEYVLFYYSNLSVPTGRFQNRSHLVGDTFHNDGSLLLQDVQVQADQGTIYCE 120
QY 118 IRLKGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIF-SGRR 176
Db 121 IRLKNESVMVMKKPVLEWVLPPEPKDLRVRGDTTQMRCISIQSTEEKRVTKVNMWPFSSGSH 180
QY 177 AKEEIVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSI 236
Db 181 TEEETVLSYDSNMRSG--KFQSLGRFRNRVLDLTDISRNDGSIKLTQVKESDRGIYTCSI 238
QY 237 HLGNLVFKKKTIVLHVSPEEPRTLVTPAALRPL-----VLGGNQLVIVIGIVCATILLLP 290
Db 239 YVGKLESRKKTIVLHVVDQDEFQRTISPTF--PTDKGQQGLNGNLVIVIGIVCATFLLLP 296
QY 291 VLILIVKKTGCKNSVNSTVLVK--NTKKTNPKEIKPCHFERCEGEKHIYSPPIIIVREV 347
Db 297 VLILIVKAKWNKSSVSSMASVKSLENKEKINP-----EKHIYSSITTWET 342
QY 348 IEEEEPESEKSEATYTMHPVWPVWPSLRSDRNNLSLEKKS 383
Db 343 TERGISGE-SEGTYMTNPNVWPS--SPKASSLVRSS 375

RESULT 6
Q9YGV5
ID Q9YGV5 PRELIMINARY; PRT; 335 AA.
AC Q9YGV5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ChT1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077161; PubMed=9862345;
RA Chretien I., Marcuz A., Courtet M., Katevuo K., Vainio O., Heath J.K.,
RA White S.J., Du Pasquier L.;
RT "CTX, a Xenopus thymocyte receptor, defines a molecular family
conserved throughout vertebrates."
RL Eur. J. Immunol. 28:4094-4104(1998).
DR EMBL; AF061023; AAD17523.1; -.
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 335 AA; 36561 MW; 071A313C3CE6DCA0 CRC64;

Query Match 9.6%; Score 198; DB 13; Length 335;
Best Local Similarity 22.1%; Pred. No. 1.2e-09;
Matches 88; Conservative 74; Mismatches 158; Indels 78; Gaps 17;

Db 283 PKSRTSTARSY-----IGSNHSSLGSMSPSNMEGYSKTQ 317

RESULT 11

Q9NR99 PRELIMINARY; PRT; 2828 AA.
AC Q9NR99;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Adlican.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Crowl R.M., Luk D.;
RT "Identification of the gene encoding Adlican, a novel protein
expressed in human arthritic tissues."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF245505; AAF86402.1; -.
DR HSSP; P56276; 1TLK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00047; Ig; 12.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR SMART; SM00408; IGC2; 10.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 3.
DR PROSITE; PS50835; IG_LIKE; 12.
KW Immunoglobulin domain.
SQ SEQUENCE 2828 AA; 312291 MW; A18377D8554F1FE1 CRC64;

Query Match 8.1%; Score 167; DB 4; Length 2828;
Best Local Similarity 21.8%; Pred. No. 1.5e-05;
Matches 87; Conservative 74; Mismatches 149; Indels 90; Gaps 20;

QY 42 CVFQST--EDKCFKIDWTLSPG--EHAKD-EYVLYYSNL-----SVP 80
Db 2221 CVARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVFYGGDLKVDCAVATGLPNPEISWSLP 2280
QY 81 IGRFQNRVHLMGD-----ILCNDGSLLDQVQVQADQGTIYC--EIRL-KGESQVFK 129
Db 2281 DGSLVNSFMQSDSGGRTKRYVVFNNGLTFNEVGMREEDGYTCFAENQVQKDEMRVRVK 2340
QY 130 AVVLHVLPEEPKELMHV--GGLIQMGCVFQSTEVKHTVKVEWIFSGRAKEEIVFRYH 187
Db 2341 VVTAPATIRNKTYLAVQVPYGDVVTVAC---EAKGEMPKVTWLSPTNKV----- 2387
QY 188 KLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHGLNLFVKTI 247
Db 2388 -IPTSEKXQIY-----QDGTLLIQAKRSDSGNYTCLVRNSAGEDRKIV 2431
QY 248 VLHVSPEPRTLVP---AALRPLVLGNQLVI---IVGIVCATIL-LPLVLILIVKTC 300
Db 2432 WIHVNVQPPKINGNPNTITVREIAAGGSRKLIDCKAEGIPTPRVLWAFPEGVVLPAFY 2491
QY 301 GNKSSV--NSTVLVKNTKTNPEIKEKPCHEPERCEGEKHIYPIIIVREVIEE---EEP-S 354
Db 2492 GNRITVHGNGSLDIRSLRKS--DSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPI 2549
QY 355 EKSEATYMTMHPV-----WPSLRSDRNNLSLEKSG 384
Db 2550 EK--ITANAGHTISLNCSAAGTPTPSLVVWLPNGTDLQSG 2587

RESULT 12

Q9TU80 PRELIMINARY; PRT; 319 AA.
AC Q9TU80;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cossackie-adenovirus-receptor homolog (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed German shepherd; TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Cossackie-adenovirus-receptor and alpha v-integrin does
not correlate with adenovector targeting in vivo indicating anatomical
vector barriers."
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109645; AAF01256.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
FT NON TER 319 319
SQ SEQUENCE 319 AA; 35422 MW; 85C63A6EC7986965 CRC64;

Query Match 7.9%; Score 164; DB 6; Length 319;
Best Local Similarity 22.6%; Pred. No. 1.4e-06;
Matches 91; Conservative 61; Mismatches 146; Indels 104; Gaps 19;

QY 5 LKLILLPLLDYSLGLNDLNVSPPELTVH--VGDSALMGCVFQ-STEDKCFKIDWTLS 61
Db 5 LRFVLLCGVADFT--RSLSITTEQMIKAKGETAYLPCKFTLSPEQGLDIEWLLSP 61
QY 62 GEHAKDEVVLYYSNLSPVIGRFQ---RVHL-MGDILCNDGSLLDQVQVQADQGTIYC 117
Db 62 ADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKSADASINVTNLRSLDGTGYQCK 121
QY 118 IRLKGESQVFKKAVVLHVLPEEPKELMHVHVGGLIQMGCVF---QSTEVKHTVKVEWIFS 173
Db 122 V--KKAPGVGNKKIQLTVL-VKPSGIRCVYDGESEIIGNDFKLKCEPKESLPQYEW--- 175
QY 174 GRRAKEEIVFRYYHKLKRMVSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYT 233
Db 176 -----QKLSNSQKTPPSWS-----TDMTSPV-----ISIKNASTEYSGTI 211
QY 234 CSIHGLNLFVKTIIVLHVSPE--EPRTLVTTPAALRPLVLGNQLVIIVGIVCATILLPV 291
Db 212 C-----TVTNRVGSDQCQLRLNVVPPSNRAGIAG---AVVG-----ILLALV 251
QY 292 LILIVKTKCGNKSNNSTVLVKNTKTNPEIKEKPCHEPERCEGEKHIYPIIIVREVIEE 351
Db 252 LIGFIVFCC-----RKKREKYEKEVHD-----IRED 280
QY 352 EPSEKSEATYMTMHPVWPSLRSDRNN--SLEKSGGGMPTQ 391
Db 281 VPPLKSRSTARSY-----IGSNHSSLGSMSPSNMEGYSKTQ 317

RESULT 13

Q9H6B4 PRELIMINARY; PRT; 373 AA.
ID Q9H6B4
AC Q9H6B4;

